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GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
               Copyright
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OM protein - protein search, using sw model

October 14, 2005, 15:51:19; Search time 38.4375 Seconds (without alignments) 50.310 Million cell updates/sec Run on:

US-10-614-959-10 29

1 TYAMH 5 score: Sequence: Title: Perfect s

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2105692 segs, 386760381 residues Searched:

2105692

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp20028:* geneseqp2003a8:* geneseqp2003b8:* geneseqp20048:* geneseqp1980s:* geneseqp1990s:* geneseqp2000s:* geneseqp2001s:* A Geneseq 16Dec04:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

u.	Anti-fact	Aspergill	Aspergill	Amino act	HCV El an	HCV E1 an	Protein e	Pseudomon	Bacterial	Human OR-	Human olf	Human pro	A. oryzae	A. oryzae	Aspergill	Aspergill	Human 1mm	Peptide #	Peptide #	Human bon	Human bra	Human liv	Human pep	Novel hum	Human DNA
Description	Aay79068 1	Aab14789 1	-	Aag65570 /	_	6	7	Abo77482		Aag72483 I						Aab14782 1		Abb40299 1	Aam33985 1	Aam73798 1	Aam61093 1	_	_		Abg92629 1
QI	AAY79068	AAB14789	AAB14784	AAG65570	ABG76537	ABG76559	ABU24807	AB077482	ADN27332	AAG72483	AAG71475	ADR10293	AAY50844	AAY50835	AAB14781	AAB14782	AAM82576	ABB40299	AAM33985	AAM73798	AAM61093	ABG55546	ABG43685	AAU18208	ABG92629
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Length	ß	7	12	120	121	128	206	258	278	307	321	531	069	9	703	703	46	67	67	67	67	67	67	79	79
% Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	89.7	89.7	89.7	89.7	89.7	89.7	89.7	89.7	89.7
Score	29	29	29	29	29	29	29	29	29	29	29	29	29	29	29	29	26	26	26	26	26	26	26	26	26
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79 7 ADC25346 89 5 ABG68752 1162 5 ABG68752 1173 5 ABG68756 1194 7 ADE08218 205 7 ADE08218 2105 7 ADE08219 221 6 ADA55412 221 6 ADA55412 221 6 ADA55412 238 7 ADE08019 242 5 ABB49910 242 5 ABB49910 242 5 ABB49910 244 7 ADG91423 370 4 AAG91423 370 4 AAG91423 370 7 ADE57186 501 8 ADE57186 502 7 ADE57180		Abo63767 Klebsiell Adf08003 Bacterial Ado47242 Rabbit cy Aae26192 Human cyt Ade57186 Human Pro Ade57190 Human Pro
	ADC25346 ABG68752 ABG68756 ADB08218 ADB08218 ADB08219 ABB91152 ADA55412 ADA55412 ABH49910 ABH49910 ABH49910 AAG14642 AAG96869 ABH49910	ABO63767 ADF08003 ADO47242 AAE56192 ADE57186 ADE57190
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ALIGNMENTS

Complementarity determining region 1; CDR1; antibody; Gla domain; factor IX/IXa; blood coagulation; deep venous thrombosis; arterial thrombosis; unstable angina; post myocardial infarction; coronary artery bypass graft; CABG; stroke; tumour growth; metastasis; percutaneous transluminal coronary angioplasty; PTCA; inflammation; septic shock; hypotension; adult respiratory distress syndrome; ARDS; arterial fibrillation; disseminated intravascular coagulopathy; DIC. Anti-factor IX/IXa antibody H chain V domain CDR1 amino acid sequence. AAY79068 standard; peptide; 5 AA. (first entry) 12-JUN-2000 AAY79068;

99WO-US019453. 98US-0098233P. 99US-0122767P. WO200012562-A1. Homo sapiens. 26-AUG-1999; 28-AUG-1998; 03-MAR-1999; 09-MAR-2000

(GETH) GENENTECH INC

Devaux B, Eaton DL, Hass PE, Adams CW, Suggett S;

Kirchhofer D;

Judice JK,

Novel human anti-Factor IX/IXa antibodies against IX/IXa gamma-carboxyglutamic acid domains useful as anti-coagulant in thrombosis, stroke, and post myocardial infarction. WPI; 2000-256595/22.

Claim 2; Fig 2; 84pp; English.

This sequence represents a complementarity determining region 1 (CDR1) of the heavy chain variable domain of a human anti-factor IX/IXa Gla domain antibody. Factor IXa is a vitamin K dependent plasma serine protease that participates in the blood coagulation pathways. The Gla domain of factor IXa and its zymogen factor IX contains important structural determinants for interaction with high affinity binding sites on vascular endothelial

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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to two novel glutaminases (AAB14781, AAB14782) from Aspergillus oryaae KBN616 and Aspergillus sojae BA-104 respectively which have molecular weights of approximately 73 kD (as determined by gel filtration). The enzymes have an optimum temperature of approximately 50 degrees Celsius, and an optimum pH of about 8.5. The glutaminases catalypee the conversion of L-glutamine to L-glutamic acid, and may be used in the production of fermented foodstuffs such as soy sauce and miso. Sequences AAB14787-B14789 represent fragments of Aspergillus oryzae KBN616 glutaminase which were used as the basis for the design of degenerate PCR primers AAA72205, AAA72207 and AAA72209. These primers were used in the isolation of genomic DNA encoding Aspergillus oryzae
         the treatment or prophylaxis of thrombotic or coagulopathic diseases or disorders in a mammal for which inhibiting a FIX/IXa mediated event is indicated, e.g. deep venous thrombosis, arterial thrombosis, unstable angina, post myocardial infartion, post surgical thrombosis, coronary artery bypass graft (CABG), percutaneous transluminal coronary angioplasty (PTCA), stroke, tumour growth, invasion or metastasis, inflammation, septic shock, hypotension, adult respiratory distress syndrome (ARDS), arterial fibrillation and disseminated intravascular coagulopathy (DIC)
                                                                                                                                                                                                                                                                                                                                                                                                                             Glutaminase, Aspergillus oryzae KBN616; glutamic acid synthesis;
fermentation; foodstuff production; miso; soy sauce; peptide fragment;
                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                     Aspergillus oryzae KBN616 glutaminase peptide, SEQ ID NO:12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity 100.0%; Score 29; DB 3; Length 7; Similarity 100.0%; Pred. No. 1.8e+06; 5; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                        Length 5;
                                                                                                                                                                                                  0; Indels
                                                                                                                                                                       100.0%; Score 29; DB 3; I
100.0%; Pred. No. 1.8e+06;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        new glutaminase and its preparation.
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                                                                                                                                                                                                                                                                                                                         AAB14789 standard; peptide; 7 AA.
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                                                                                                                                                         Query Match
Query Match
Best Local Similarity 100.0.
                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-477931/42.
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Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Aspergillus oryzae
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                                                                                                                                              Sequence 5 AA;
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Gaps . 0

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        determined for three V8 protease fragments (P1-P3) of Aspergillus oryzae KBN616 glutaminase in an exemplification of the invention
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                                                                                                                                                                                                                                                                                                             Aspergillus oryzae KBN616 glutaminase peptide fragment, SEQ ID NO:6.
                                                                                                                                                                                                                                                                                                                                                        Glutaminase; Aspergillus oryzae KBN616; glutamic acid synthesis; fermentation; foodstuff production; miso; soy sauce; V8 protease digestion.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A new glutaminase and its preparation.
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                                                                                                                                                                  AAB14784 standard; peptide; 12 AA
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                                                                                                                                                                                                                                                                  06-DEC-2000 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Aspergillus oryzae.
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les 5; Conserv
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1 TYAMH
                                     TYAMH
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                                                                                                                                                                                                                  AAB14784;
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virus

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Homo sapiens.
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Vaccine
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Matches
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                                                                                                                                                                                                                    The invention relates to producing gene libraries, comprising immunoglobulin light and heavy variable region. The method involves selecting light chain that binds with the heavy chain product to produce a functional conformation, producing a gene library comprising a collection of these light chain variable genes, and combining with gene library of heavy chain variable genes. The method is used for production of gene and antibody libraries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human, HCV, hepatitis C virus; El antigen, monoclonal antibody, vaccine,
hepatotropic, Fab, hypervariable region; E2 antigen, antibody.
                                                                                                                                                         Producing gene libraries and antibody libraries, involves selecting a
light chain that binds to a heavy chain product to produce a functional
formation, and producing a gene library of the light chain variable
                                                                                                      Shinohara M, Takahashi M;
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                                                                                                                                                                                                                                                                                                             100.0%; Score 29; DB 4; Length 120; 100.0%; Pred. No. 72;
                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                      Iba Y, Morino K,
                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                      (MEDI-) MEDICAL & BIOLOGICAL LAB CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HCV El antigen monoclonal antibody #25.
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                                                                                                                                                                                                     Examples; p 171; 181pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-JAN-2001; 2001US-0260889P.
                                                   22-FEB-2001; 2001WO-JP001298
                                                                     22-FEB-2000; 2000JP-00050543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-JAN-2002; 2002WO-SE000044
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                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                     Local Similarity 100.
                                                                                                      Kurosawa Y, Akahori Y,
Okuno Y, Shiraki K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-608502/65.
                                                                                                                                2001-565420/63.
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TYAMH 35
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                                                                                                                                          N-PSDB; AAH47734
                                                                                                                                                                                                                                                                                            Sequence 120 AA;
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                 WO200162907-A1
Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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                                  30-AUG-2001
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                                                                                                                                                                                                                                                                                                             Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; HCV; hepatitis C virus; El antigen; monoclonal antibody; vaccine; hepatotropic; Fab; hypervariable region; E2 antigen; antibody.
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                                                                                                                                                                             The invention relates to a human monoclonal antibody or its antigen binding fragments, which exhibit immunological binding affinity for a hepatitis C virus (HCV) B1 antigen, comprising an amino acid sequence homologous to the binding portion of a human antibody Fab molecule from combinatorial antibody library. The vaccine composition comprising the antibodies or antigen binding fragments againet HCV B1 or B2 antigen or its hypervariable region is useful in treating or preventing HCV infection in a subject. Sequences ABG76513-ABG76568 represent human monoclonal antibodies against HCV B1 antigen
Vaccine comprising a human monoclonal antibody against hepatitis C virus (HCV) El or E2 antigen, useful for treating or preventing HCV infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HCV El antigen monoclonal antibody #47.
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                                                                                                                    Disclosure; Page 36; 64pp; English
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Similarity 100.0%;
5; Conservative 0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-JAN-2001; 2001US-0260889P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Persson MAA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-NOV-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-608502/65.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  . 33 TYAMH 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 TYAMH 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 121 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 128 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200260954-A1
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                                                                                                                                                                                                                                                                                                                                                       New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                       Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                                                                                                                                                                                                                                                         Zyskind JW;
Xu HH;
                Gaps
                ö
                                                                                                                                                                                                                                                                                                         Ohlsen KL,
Forsyth RA,
                Indels
                                                                                                                                       Protein encoded by Prokaryotic essential gene #10334.
                ö
                                                                                                                                                                                                                                                                                                         Haselbeck R,
Yamamoto R,
       77;
               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                        Claim 25; SEQ ID NO 52731; 1766pp; English
       Pred. No.
                                                                                       ABU24807 standard; protein; 206 AA
100.08; Pre-
                                                                                                                                                                                                                                                                                                         Malone C,
Carr GJ,
                                                                                                                                                                                                                                                ; 2001US-00948993.
; 2001US-0342923P.
; 2002US-00072851.
; 2002US-0362699P.
                                                                                                                                                                                                                        21-MAR-2002; 2002WO-US009107.
                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                        (ELIT-) ELITRA PHARM INC.
                5; Conservative
                                                                                                                                                                        Clostridium botulinum
                                                                                                                                                                                                                                                                                                         Zamudio C,
Trawick JD,
                                                                                                                                                                                                                                                                                                                                 WPI; 2003-029926/02
       Best Local Similarity
                                               TYAMH 36
                               TYAMH 5
                                                                                                                                                                                                                                                                                                                                          N-PSDB; ACA28677
                                                                                                                                                                                       WO200277183-A2
                                                                                                                                                                                                                                                06-SEP-2001;
25-OCT-2001;
08-FEB-2002;
                                                                                                                                                                                                                                        21-MAR-2001;
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                                                                                                                        19-JUN-2003
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                                                                                                        ABU24807;
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                                               32
                                                                                                                                                                                                                                                                                                         Wang L,
Wall D,
               Matches
                                                                       RESULT 7
                                                                                 ABU24807
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The invention relates to an isolated nucleic acid compilating any one of the invention relates to an isolated nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense concleic acid, (2) a host cell containing the vector; (3) an isolated conflicted acid; (2) a host cell containing the vector; (3) an isolated conflicted prolypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation, or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture compound that inhibits proliferation of an organism; or tall antibits proliferation of a proliferation of an organism. The antisense nucleic acids are useful for cellular proliferation of an organism. The antisense nucleic acids are useful for for cellular proliferation to isolate candidate molecular acids rational for for cellular proliferation to isolate candidate molecular acids are proliferational for for cellular proliferation to solational conditional control cellular proliferation to solational conditional cellular proliferation to solational candidates and cellular proliferation to conditional candidates cellular proliferation to condit and cellular proliferation of ce ö drug discovery programs, or for screening homologous nucleic acids invention relates to an isolated nucleic acid comprising any

Sequence 258 AA;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              infection, and in detection of P. aeruginosa sequences or other sequences of Pseudomonas species using biochip technology. Sequences ABO57826-88084396 represent P. aeruginosa polypeptides of the invention. Note: The sequence data for this patent did not form part of the printed specification but, was obtained in electronic format from USPTO at
required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the printed patent directly expecification, but was obtained ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide, useful as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from bacterial infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to Pseudomonas aeruginosa polypeptides and the polynucleotides encoding them. The sequences are useful in diagnosis and therapy of pathological conditions, as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from a bacterial infection, for evaluating a compound, such as a polypeptide, for the ability to bind a P. aeruginosa nucleic acid, as components of effective antibacterial targets, as targets for antibacterial drugs, including anti-P. aeruginosa drugs, as templates for recombinant production of P. aeruginosa-derived peptides or polypeptides, as target components for diagnosis and/or treatment of P. aeruginosa-caused
                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.
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0
                                                                                                                                                                    Length 206;
                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bush D;
                                                                                                                                                                  100.0%; Score 29; DB 6; L
100.0%; Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; SEQ ID NO 26228; 455pp; English
                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rubenfield MJ, Nolling J, Deloughery C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pseudomonas aeruginosa polypeptide #9657.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GENO-) GENOME THERAPEUTICS CORP
                                                                                                                                                                                                                                                                                                                                                                          ABO77482 standard; protein; 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seqdata.uspto.gov/sequence.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-00252991.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98US-0074788P.
98US-0094190P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-615309/58.
                                                                                                                                                                                     Local Similarity
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TYAMH 34
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                                                                                                                                   Sequence 206 AA;
                                                                                                                                                                                                                                              1 TYAMH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-FEB-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                              ABO77482;
                                                                                                                                                                                                                                                                               30
                                                                                                                                                                    Query Match
                                                                                                                                                                                           Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                         RESULT 8
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The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polymucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant with the such as maize or soybean. The method of producing a transformed plant when the a maize or soybean. The method of producing a plant with the recombinant DNA construct and growing the transformed plant, where the polymucleotide or polypeptide is useful for improving plant properties. The recombinant DNA construct is useful for producing plants with the recombinant DNA construct is useful for producing plants with increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of homologous recombination, modified seed oil or protein yield and/or content, improved plant growth and development under at least one stress condition, improved lighin production or improved galactomannan
                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.
                                                                                                                                                                                                                                                                                                                                      Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis; pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomannan; bacterial polypeptide.
                                      Gaps
                                     ô
   Length 258;
100.0%; Score 29; DB 7; Length 25
100.0%; Pred. No. 1.6e+02;
.ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Goldman BS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 9985; 122pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chen X,
                                                                                                                                                                                                ADN27332 standard; protein; 278 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hinkle GJ, Slater SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-FEB-2003; 2003US-00369493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-FEB-2002; 2002US-0360039P
                                                                                                                                                                                                                                                                                                      Bacterial polypeptide #9985.
                                                                                                                                                                                                                                                                     (first entry)
                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HINKLE G J.
SLATER S C.
CHEN X.
GOLDMAN B S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2004-061375/06.
                  Local Similarity
tes 5; Conserv
                                                                                                  201 TYAMH 205
                                                                        'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US2003233675-A1.
                                                                        1 TYAMH
                                                                                                                                                                                                                                                                     02-DEC-2004
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                                                                                                                                                                                                                                    ADN27332;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria.
   Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HINK/)
(SLAT/)
(CHEN/)
(GOLD/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAOY/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cao Y,
                                 Matches
                                                                                                                                                             RESULT 9
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the present sequence is a polypeptide encoded by one of 344 newly mined human genes. It was used as a query sequence in a database search of charactory receptor (OR) like sequences. The invention relates to isolated polymucleotides encoding polypeptides involved in olfactory sensation.

The polymucleotides can be used in screening for olfactory agonists and antagonists. The methods allow for the determination of primary scents and the identification of the odour receptors used to detect these primary scents. The methods also enable determination of secondary scents primary scents. The methods also enable determination of secondary scents conduction of a scent representation (also called a scent fingerprint construction of a scent representation (also called a scent fingerprint in the present of a composition with the receptors, and can be used interaction pattern of a composition with the receptors, and can be used to interaction pattern of a composition with the receptors, and can be used to interaction pattern of a composition with the receptors, and can be used to interaction pattern of a composition with the receptors, and can be used to interaction pattern of a composition with the receptors.
                                                                                                                                                                               ö
production. This sequence represents a bacterial polypeptide used in the scope of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at seqdata.uspto.gov/sequence.html.
                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human, olfactory receptor; OR; primary scent determination; secondary scent determination; polypeptide library; odour receptor; scent profile; scent fingerprint; scent representation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New polynucleotides which encode polypeptides involved in olfactory sensation for identifying olfactory agonists and antagonists.
                                                                                                                                                                               ö
                                                                                                                                        Length 278;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human OR-like polypeptide query sequence, SEQ ID NO: 2164.
                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fuchs T,
                                                                                                                                     100.0%; Score 29; DB 8; L
100.0%; Pred. No. 1.7e+02;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glusman G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 6; Page 1455-1456; 1857pp; English.
                                                                                                                                                                                                                                                                                                                                                          AAG72483 standard; protein; 307 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lancet D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (DIGI-) DIGISCENTS.
(YEDA ) YEDA RES & DEV CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-OCT-2000; 2000WO-US027582.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-OCT-1999; 99US-0158615P.
24-FEB-2000; 2000US-0184809P.
                                                                                                                   Query Match
Best Local Similarity luv.
5, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Smith D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-290713/30
                                                                                                                                                                                                                                                           220 TYAMH 224
                                                                                                                                                                                                                      1 TYAMH 5
                                                                                                  Sequence 278 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200127158-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bellenson J,
                                                                                                                                                                                                                                                                                                                                                                                                                                        31-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                 AAG72483;
                                                                                                                                                                                                                                                                                                                       RESULT 10
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4; Length 307;

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100.0%; Score 29;

Sequence 307 AA;

· Query Match

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New 1995 cDNA, useful for treating osteoporosis, neurological diseases, Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.
                                                                                                       human; oligo-capping method; diagnostic marker; gene therapy; osteoporosis; neurological disease; Alzheimer's disease; Parkinson's disease; dementia; short memory; cancer; sense or motor function; emocional reaction; fear response; panic; osteopathic; neuroprotective; nootropic; antiparkinsonian; cytostatic;
                                                                              Human protein useful for treating neurological disease Seq 3799.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 3799; 2686pp; English.
                                                                                                                                                                                                                                                                                                                                                           (REAS-) RES ASSOC BIOTECHNOLOGY,
                                                                                                                                                                                                                                                                                                                 14-FEB-2003; 2003JP-00102207. 09-MAY-2003; 2003JP-00131452.
                                                                                                                                                                                                                                                                                        12-FEB-2004; 2004EP-00003145.
                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                     Isogai T, Yamamoto J,
Wakamatsu A, Ishii S,
                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2004-583265/57.
                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; ADR08337
                                                                                                                                                                                                                                 EP1447413-A2.
                                                                                                                                                                             tranquiliser.
                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                            18-AUG-2004.
                                                     04-NOV-2004
                           ADR10293;
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               8
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                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence is an olfactory receptor which is encoded by one of a number of novel polynuclectides. The polynuclectides can be used in screening for olfactory agonists and antegonists. The methods allow for the determination of primary scents and the identification of the odour receptors used to detect these primary scents. The methods also enable determination of secondary scents and the identification of combinations of odour receptors that are involved in detecting such secondary scents. This enables the construction of a scent representation (also called a scent fingerprint or scent profile), which may be used to re-create and edit scents. Libraries of olfactory receptors are useful for determining the interaction pattern of a composition with the receptors, and can be used for determining differences in the olfactory faculties of different
                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                           Human, olfactory receptor, OR; primary scent determination,
secondary scent determination; polypeptide library; odour receptor;
scent profile; scent fingerprint; scent representation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New polynucleotides which encode polypeptides involved in olfactory sensation for identifying olfactory agonists and antagonists.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fuchs T, Yanai I;
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                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 29; DB 4; Length 321; 100.0%; Pred. No. 2e+02; ive 0; Mismatches 0; Indels
                           Indels
                                                                                                                                                                                                                                 Human olfactory receptor polypeptide, SEQ ID NO: 1156.
            Pred. No. 1.9e+02;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Glusman G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 11; Page 674-675; 1857pp; English
                                                                                                                                                  AAG71475 standard; protein; 321 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lancet D,
100.0%; Pre-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (DIGI-) DIGISCENTS.
(YEDA ) YEDA RES & DEV CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                   06-OCT-2000; 2000WO-US027582.
                                                                                                                                                                                                                                                                                                                                                                                                                                         24-FEB-2000; 2000US-0184809P.
                                                                                                                                                                                                                                                                                                                                                                                                                               99US-0158615P
                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.
           Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bellenson J, Smith D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-290713/30.
                                                                              154 TYAMH 158
                                                     1 TYAMH 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 321 AA;
                                                                                                                                                                                                                                                                                                                                             WO200127158-A2.
                                                                                                                                                                                                                                                                                                                    Homo sapiens.
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                                                                                                                                                                            AAG71475;
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Otsuki T;

Nishikawa T, Isono Y, Sugiyama T, Nagai K, Irie R;

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This invention relates to novel, isolated full length human cDNA molecules and the encoded proteins thereof. Specifically, it refers to CDNA clones obtained by an oligo-capping method, where none of these clones are identical to any known human mRNAs. The present invention describes an immunoassay to identify agonists and antagonists, as well as antibodies, antibodies, antisense molecules and siRNAs that can all be used to bind to and modulate expression of the CDNA molecules. As such, these con morbid states. In particular, they are useful in gene therapy for treating osteoporosis, neurological disease, Alzheimer's disease, Parkinson's disease, dementia, short memory and various cancers, as well as for maintaining equilibrium of sense or motor function, and for treating emotional reaction, fear response and panic. Accordingly, they exhibit osteopathic, neuroprotective, noctropic, antiparkinsonian, encoded by a full length human cDNA sequence of the invention. NOTE: This sequence is not given in the sequence listing of the specification but can be obtained on CD-ROM from the European Patent Office, Vienna Sub-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY50844 standard; protein; 690 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity 100.0%;
5; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54
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AAY50844
ID AAY50
XX
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ADR10293 standard; protein; 531 AA.

RESULT 12

ADR10293

169 TYAMH 173

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Protein Peptide

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This invention describes a novel glutaminase enzyme isolated from Aspergillus oryzae which catalyses the decomposition of glutamine to glutamic acid and ammonia. The purified glutaminase and determined partial amino-acid sequence can be used for enhancing taste particularly in glutamic acid-converting food processing to give e.g. seasoning sauces and pastes as well as other seasoning materials. The gene thus obtained can be applied as probe for hybridization providing the gene-containing DNA fragments from genome and cDNA libraries of A. oryzae and A. nidulans, and subsequently modified glutaminase-producing breed. The novel strain of A. oryzae is a highly active because of its somatic secreting ability. This sequence represents the A. oryzae glutaminase enzyme described in the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Aspergillus oryzae-originated glutaminase and partial amino-acid sequences for enhancing taste particularly in glutamic acid-converting food processing to make e.g. seasoning sauces and pastes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Glutaminase; Aspergillus oryzae KBN616; glutamic acid synthesis; fermentation; foodstuff production; miso; soy sauce.
                Glutaminase, decomposition, glutamine, glutamic acid, ammonia;
taste enhancer, seasoning, sauce, paste.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nagasaki H, Yuasa A, Kataoka J, Kitamoto K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 29; DB 3; I 100.0%; Pred. No. 4.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                      1. .20
/label= signal_peptide
21. .690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Aspergillus oryzae KBN616 glutaminase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim la; Page 41-44; 74pp; Japanese
                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB14781 standard; protein; 703 AA.
                                                                                                                                                                                                                                                                                                                                                                              98JP-00292443.
                                                                                                                                                                                                                                                                                                  99WO-JP002455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                             (AJIN ) AJINOMOTO CO INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-053292/04.
                                                                           Aspergillus oryzae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Aspergillus oryzae.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAZ43677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 690 AA;
                  Glutaminase,
                                                                                                                                                                                                                    WO9960104-A1
                                                                                                                                                                                                                                                                                                12-MAY-1999;
                                                                                                                                                                                                                                                                                                                                        15-MAY-1998;
11-SEP-1998;
14-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                   30-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Koibuchi K,
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                                                                                                                                                                                                                                                            25-NOV-1999
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                                                                                                                                    Peptide
                                                                                                                                                                            Protein
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This invention describes a novel glutaminase enzyme isolated from Aspergillus oryzae which catalyses the decomposition of glutamine to glutamic acid and ammonia. The purified glutaminase and determined partial amino-acid sequence can be used for enhancing taste particularly in glutamic acid-converting food processing to give e.g. seasoning sauces and pastes as well as other seasoning materials. The gene thus obtained can be applied as probe for hybridization providing the gene-containing DNA fragments from genome and CDNA libraries of A. oryzae and A. nidulans, and subsequently modified glutaminase-producing breed. The novel strain of A. oryzae is a highly active because of its somatic secreting ability. This sequence represents the A. oryzae glutaminase enzyme described in the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Aspergillus oryzae-originated glutaminase and partial amino-acid sequences for enhancing taste particularly in glutamic acid-converting food processing to make e.g. seasoning sauces and pastes.
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                                                                                                                 Glutaminase; decomposition; glutamine; glutamic acid; ammonia; taste enhancer; seasoning; sauce; paste.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nagasaki H, Yuasa A, Kataoka J, Kitamoto K;
                                                                                                                                                                                                                                       1. .20
/label= signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 3; Page 52-55; 74pp; Japanese.
                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY50835 standard; protein; 690 AA

 A. oryzae glutaminase protein #1.

                                                                           A. oryzae glutaminase protein #2
                                                                                                                                                                                                                                                                                                                                                                                                                                           98JP-00134080.
98JP-00258974.
98JP-00292443.
                                                                                                                                                                                                                                                                                                                                                                                                     99WO-JP002455.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99JP-00089157
                                   (first entry)
                                                                                                                                                                                                                                                                             21. .690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (AJIN ) AJINOMOTO CO INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-053292/04.
                                                                                                                                                                            Aspergillus oryzae.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 690 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAZ43684
                                                                                                                                                                                                                                                                                                                                                                                                                                         15-MAY-1998;
11-SEP-1998;
14-OCT-1998;
                                   24-FEB-2000
                                                                                                                                                                                                                                                                                                                       WO9960104-A1
                                                                                                                                                                                                                                                                                                                                                                                                     12-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Koibuchi K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-MAR-1999;
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Gaps

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Indels

423

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AAY5083

8X4X5X8

Query Match

Matches

Length 690;

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This sequence represents a novel glutaminase from Aspergillus oryzae KBN616. The invention relates to two novel glutaminases (AAB14781, AAB14782) from Aspergillus oryzae KBN616 and Aspergillus sojae BA-104 respectively which have molecular weights of approximately 73 kD (as determined by gel filtration). The enzymes have an optimum temperature of approximately 50 degrees Celsius, and an optimum pH of about 8.5. The glutaminases catalyse the conversion of L-glutamine to 1-glutamic and an approximately 50 degrees the conversion of fermented foodstuffs such as soy
               Location/Qualifiers
34. .703
/note= "Mature glutaminase; specifically claimed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
100.0%; Score 29; DB 3; Length 703;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                    A new glutaminase and its preparation.
                                                                                                                                                                                                                                                                                                                                                Claim 2; Page 15-17; 27pp; Japanese.
                                                                                                                                                98JP-00347127.
                                                                                                                                                                                 98JP-00347127.
                                                                                                                                                                                                                (AICH-) AICHI KEN PREFECTURE. (ICHI-) ICHIBIKI KK.
                                                                                                                                                                                                                                                                WPI; 2000-477931/42.
N-PSDB; AAA72204.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 703 AA;
                                                                               JP2000166547-A.
                                                                                                                                                07-DEC-1998;
                                                                                                                                                                                 07-DEC-1998;
                                                                                                                20-JUN-2000.
                 Key
Protein
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Search completed: October 14, 2005, 16:12:37 Job time: 42.4375 secs

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0; Gaps

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

Run on: October 14, 2005, 16:02:59; Search time 6.95312 Seconds
(without alignments)
69.190 Million cell updates/sec

Title: US-10-614-959-10
Perfect BCOre: 29

Sequence: 1 TYAMH 5
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 segs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0 Maximum DB seq length: 200000000 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	heavy	heavy c	adenylate kinase (conserved hypothet	hypothetical prote	tsh protein - Esch	hypothetical prote	•	hypothetical prote	conserved hypothet	hypothetical prote	subtilis Y	B YvpB	щ			cytochrome P450 3A			lysed fla				fix23-3 protein -	probable helicase	hypothetical prote	integumentary muci	polyketide synthas	Ig heavy chain V r
	ឧ	M3HUGA	A35676	D71184	B83290	H71347	154632	T34500	150675	H86403	E90215	T22924	AD1165	AD1524	A29487	A34236	A34101	A25222	E82423	A84425	B64679	GNLJGA	GNLJGB	829358	S18955	F84517	T21706	T30886	T30228	S26887
	四	н	~	7	~	~	~	~	~	~	~	N	~	~	7	~	н	7	7	~	N	н	Н	~	7	~	7	~	~	0
	Length	122	138	196	249	1151	1377	95	196	213	222	228	242	242	501	501	502	504	609	723	801	852	852	852	996	1265	1385	1506	6260	35
	Match	100.0	100.0	100.0	100.0	100.0	100.0	89.7	89.7	89.7	89.7	89.7	89.7	89.7	89.7	89.7	89.7	89.7	89.7	89.7	89.7	89.7		89.7	89.7	89.7	89.7	89.7	89.7	86.2
	Score	29	29	29	29	29	29	56	26	26	26	26	26	26	26	26	56	26	26	26	26	26	26	56	26	26	26	26	26	25
Result	No.		7	m	4	S	9	7	80	თ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

31 TYAMH 35

8 8

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1 TYAMH

RESULT 2
A35676
Ig heavy chain precursor V-D-J region - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 28-Sep-1990 #sequence_revision 28-Sep-1990 #text_change 23-Jul-1999
C;Jate: Immunoglobulin D switching can occur through homologous recombination in human A;Reference number: A35676; MUD:90287160; PMID:2113175
A;Accession: A35676
A;Accession: A35676
A;Residues: DNA
A;Residues: 1-138 <AMI:>A;Residues: 1-138 <AMI:>A;Residues: 1-138 <AMI:>A;Conse-references: GB:M38066; NID:g185466; PIDN:AA452974.1; PID:g553407
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <INM>

heavy heavy heavy		bable heavy heavy heavy	Ig heavy chain V r Ig heavy chain V r Ig heavy chain V r Ig heavy chain V r Ig heavy chain V r
S46473 PL0120 S17609	\$10385 \$26885 \$26886 \$29546	S53076 PH1665 PH1653 PH1646	PH1644 PH1645 E33936 PH1667 S46390
6 9 9 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5			1009 1111 1114 1114 22
86.2 86.2 86.2	88 88 88 88 88 88 88 88	8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
25 25 25	22222	2222	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2
30 31 32	. W W W W W 4 W W	7 8 8 8 4 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4

ALIGNMENTS

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hypothetical protein TP0245 - syphilis spirochete
C;Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
C;Accession: H7134.
C;Accession: H7134.
C;Accession: H7134.
E;Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McDo, they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998
A;Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A;Reference number: A71250; MUID:98332770; PMID:9665876
A;Accession: H71347
A;Molecule type: DMA
A;Accession: H71347
A;Accession: H71347
A;Accession: H71347
A;Accession: H7151 DMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Residues: 1-1151 <COL>
A;Cross-references: UNIPROT:083273; GB:AE001206; GB:AE000520; NID:g3322514; PIDN:AAC6523*
A;Experimental source: strain Nichols
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Bscherichia coli
C;Species: Bscherichia coli
C;Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 09-Jul-2004
C;Datesion: 1596 #sequence_revision 07-Jun-1996 #text_change 09-Jul-2004
C;Accession: 159632
R;Provence, D.L.; Curtiss, R.
Infect. Immun. 62, 1369-1380, 1994
A;Title: Isolation and characterization of a gene involved in hemagglutination by an avi.
A;Reference number: 154632; MUID:94178945; PMID:8132344
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: DNA
*Residues 1.137 <RES.
A;Cross-references: UNIPROT:047692; GB:L27423; NID:9469235; PIDN:AAA24698.1; PID:9469236.
C;Superfamily: IgA-specific metalloendopeptidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Cross-references: UNIDROT.Q23428; EMBL:U29244; PIDN:AAC71098.1; GSPDB:GN00020; CESP:ZK
A,Experimental source: strain Bristol N2; clone ZK1248
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T34500
R;Latreille, P.
Submitted to the EMBL Data Library, June 1995
A;Description: The sequence of C. elegans cosmid ZK1248.
A;Reference number: Z21534
A;Accession: T34500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Genetics:
A;Gene: TP0245
C;Superfamily: syphilis spirochete hypothetical protein TP0245
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A;Molecule type: DNA
A;Residues: 1-95 <LAT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ademplate kinase (EC 2.7.4.3) PH1753 [similarity] - Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Species: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 12-Jul-2004
C;Accession: D71184
C;Accession: D7184
C;Accesi
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B83290
conserved hypothetical protein PA2847 [imported] - Pseudomonas aeruginosa (strain PAO1)
C;Species: Pseudomonas aeruginosa
C;Species: Pseudomonas aeruginosa
C;Species: Pseudomonas aeruginosa
C;Species: Dseudomonas aeruginosa
C;Species: Dseudomonas aeruginosa
C;Species: Dseudomonas aeruginosa
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
S; Yuan, Y.; Suonome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathc
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Residues: L-249 cSTO>
A;Cosseries: preliminary
A;Molecule type: DNA
A;Residues: 1-249 cSTO>
A;Cross-references: UNIPROT:O9HZZ6; GB:AE004711; GB:AE004091; NID:g9948927; PIDN:AAG0623
A;Genetics:
A;Genetics: A;Genetics:
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                                                                    Length 138;
                                                                                                                                                     0; Indels
                                                               Query Match

100.0%; Score 29; DB 2;
Best Local Similarity 100.0%; Pred. No. 9;
Matches 5; Conservative 0; Mismatches 0
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Query Match
Best Local Similarity 80.0%;
Matches 4; Conservative

||:|| 12 TYSMH 16

1 TYAMH 5

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Rishe, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J. Submitted to GenBank, April 2001
A; Description: Sulfolobus solfataricus complete genome.
A; Reference number: A99139
A; Accession: E90215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Residues: 1.222 «KUR»
A;Cross-references: UNIPROT:Q9UX67; GB:AE006641; NID:g13813846; PIDN:AAK40980.1; GSPDB:G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Accession: AD1165
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H. D.; Jones, L.M.; Karst, U.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                       conserved hypothetical protein [imported] - Sulfolobus solfataricus C;5pecies: Sulfolobus solfataricus C;5pecies: Sulfolobus solfataricus C;5pecies: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004 C;Accession: E90215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein F58B6.8 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T22924
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A;Introns: 153/2
C;Superfamily: Caenorhabditis elegans hypothetical protein Y75B12A.2
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80.0%; Pred. No. 78;
iive 1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 26; DB 2
Pred. No. 76;
1; Mismatches
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C, Superfamily: hypothetical protein MJ0570
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Best Local Similarity 80.0%;
Matches 4; Conservative
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Matches 4; Conservative
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202 TYALH 206
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A;Map position: 5
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: O2-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: #86403
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Ji, Y.; Liu, X.; Liu, X.; Liu, X.X.; Liu, X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Titles: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: mRNA
A;Residues: 1-196 <VIE>
A;Cross-references: UNIPROT:P41263; EMBL:X77960; NID:g457778; PIDN:CAA54922.1; PID:g4577
                                                                                                                                                                                                                                                                                                                                                                                                         retinol-binding protein precursor - chicken

c;Species Gallus Gallus (chicken)

C;Species Gallus Gallus (chicken)

C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004

C;Accession: I50675; 842887

R;Vieira. A.V.; Kuchler, K.; Schneider, W.J.

DNA Cell Biol. 14, 403-410, 1995

A;Title: Retinol in avian oogenesis: molecular properties of the carrier protein.

A;Reference number: I50675; MUID:95267350; PMID:7746490

A;Accession: I50675

A;Status; preliminary; translated from GB/EMBL/DDBJ
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80.0%; Pred. No. 67;
iive 1; Mismatches 0; Indels
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Pred. No. 73;
1; Mismatches 0; Indels
                                                                                   Score 26; DB 2; Length 95;
Pred. No. 32;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Superfamily: lipocalin; lipocalin homology
F1.21/Domain: signal sequence #status predicted <SIG>
F36-195/Domain: lipocalin homology <LIP>
F35-181,91-195,141-150/Disulfide bonds: #status predicted
A;Map position: 2
C;Superfamily: Caenorhabditis elegans major sperm protein
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Best Local Similarity 80.0 Matches 4; Conservative

Query Match

C; Genetics:

|||:| 134 TYALH 138

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1 TYAMH 5

89.7%;

Query Match 89.7 Best Local Similarity 80.0 Matches 4; Conservative

1 TYAMH 5

A,Status: preliminary A,Molecule type: DNA A,Residues: 1-213 <STO>

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396 TYALH 400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 TYAMH 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C, Genetics
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AD1524
B. subtilis YupB protein homolog lin0732 [imported] - Listeria innocua (strain Clip11262 C;Species: Listeria innocua
C;Species: Listeria innocua
C;Species: Listeria innocua
C;Species: Listeria innocua
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Accession: AD1524
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
J; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitcournam, A.; Ma
Ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A;Atcheroc number: AB1077; MUD121537279; PMID:11679669
A;Accession: AD1524
A;Stetus: preliminary
A;Molecule type: DNA
A;Residues: 1-242 <GGA>
A;Accession: Calaba
A;Residues: 1-242 <GGA>
A;Cross-references: UNIPROT:Q92DT0; GB:AL592022; PIDN:CAC95964.1; PID:g16413184; GSPDB:C
C;Genetics:
A;Gene: lin0732
C;Superfamily: Bacillus subtilis hypothetical protein yvpB
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Sylvathrowner P450 3A6 (version 1) - rabbit
Notains: oxidoreductase (EC 1.....)
Cytochrome P450 3C
NiContains: oxidoreductase (EC 1.....)
CySpecies: Oxyctolagus cuniculus (domestic rabbit)
CySpecies: Oryctolagus cuniculus (domestic rabbit)
CySpecies: Oryctolagus cuniculus (domestic rabbit)
CySpecies: Oxyctolagus cuniculus (domestic rabbit)
CySpecies: Oxyctolagus cuniculus (domestic rabbit)
CySpecies: Oxyctolagus cuniculus (domestic rabbit)
RyDalet, C.; Clair, P.; Daujat, M.; Fort, P.; Blanchard, J.M.; Maurel, P.
RyDalet, C.; Clair, P.; Daujat, M.; Fort, P.; Blanchard, J.M.; Maurel, P.
A; Dalet, Complete sequence of cytochrome P450 3c cDNA and presence of two mRNA species wather complete number: A29487, MUID:88166352; PMID:3349903
A; Accession: A29487
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Cossaidus: 1-501 cDAL>
A; Cossai
A.Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mack, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.Title: Comparative genomics of Listeria species.
A.Fitle: Comparative genomics of Listeria species.
A.Reference number: AB1077; MUID:21537279; PMID:11679669
A.Accession: AD1165
A.Status: preliminary
A.Kolecule type: DNA
A.Resiques: 1-242 <GLA>
A.Resiques: 1-242 <GLA>
A.Resiques: UNIPROT:Q8Y918; GB:NC_003210; PIDN:CAC98802.1; PID:g16410113; GSPDB:A.Scherimental source: strain EGD-e
C.Genetics: A.Status and Subtilis hypothetical protein yvpB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     89.7%; Score 26; DB 2; Length 242; 80.0%; Pred. No. 83;
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191 TYSMH 195
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191 TYSMH 195
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AjGene: CYP3A6
C;Superfamily: human cytochrome P450 CYP3A5; cytochrome P450 homology
C;Keywords: chromoprotein; electron transfer; heme; iron; metalloprotein; monooxygenase;
F;301-462/Domain: cytochrome P450 homology <P45>
F;440/Binding site: heme iron (Cys) (axial ligand) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Accession: A34236
R;Potenza, C.L.; Pendurthi, U.R.; Strom, D.K.; Tukey, R.H.; Griffin, K.J.; Schwab, G.E.;
R;Potenza, C.L.; Pendurthi, U.R.; Strom, D.K.; Tukey, R.H.; Griffin, K.J.; Schwab, G.E.;
D atol. Chem. 264, 16222-16228, 1389
A;Title: Regulation of the rabbit cytochrome P-450 3c gene. Age-dependent expression and A;Reference number: A34236; MUID:89380226; PMID:2777787
A;Accession: A34236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: mRNA
A;Residues: 1-501 <POT>
A;Cross-references: UNIPROT:P11707; GB:J05034; NID:g164829; PIDN:AAA31178.1; PID:g164830
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NiContains: oxidoreductase (EC 1.....)
CiSpecies: Oryctolagus cuniculus (domestic rabbit)
CiDate: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Superfamily: human cytochrome P450 CYP3A5; cytochrome P450 homology C;Keywords: chromoprotein; electron transfer; heme; iron; metalloprotein; F;300-462/Domain: cytochrome P450 homology <P45>
F;440/Binding site: heme iron (Cys) (axial ligand) #status predicted
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80.0%; Pred. No. 1.7e+02;
ative 1; Mismatches 0; Indels
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Pred. No. 1.7e+02;
1; Mismatches 0
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                                                                                                                                                                                                          Query Match
Best Local Similarity 80.0%;
Matches 4; Conservative
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Best Local Similarity 80.0*
-hag 4; Conservative
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HV3H HUMAN STANDARD; PRT; 122 AA. 10 HV3H HUMAN STANDARD; PRT; 122 AA. 10 PV1769; DT 21-JUL-1986 (Rel. 01, Last sequence update) DT 21-JUL-1996 (Rel. 01, Last sequence update) DT 05-JUL-2004 (Rel. 44, Last annotation update) DE 19 heavy chain V-III region GA.
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25
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                                                                                                                                  October 14, 2005, 15:51:44 ; Search time 33.2812 Seconds (without alignments) 76.932 Million cell updates/sec
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Q66bk2
Q868k1
Q61mv3
Q67rr8
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059443
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                GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Q9HZZG

Q9HZZG

Q9HZZG

Q6H097

Q6 BCN4

Q8 BWR9

Q9 GAJ

Q9 GAJ

Q9 GAS

Q9 GAS
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Q66BK2
Q86SK1
Q61MV3
Q67RR8
RETB CHICK
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Maximum Match 100%
Listing first 45 summaries
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1: uniprot_sprot:*
2: uniprot_trembl:*
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29
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Maximum DB
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Controlled From N. C. Cheng Z., Nagamura Y., Baba T., Katayose Y., Sasaki T., Matsumoto T., Yamamoto K., Sakata K., Baba T., Katayose Y., Sasaki T., Matsumoto T., Yamamoto K., Sakata K., Baba T., Kanamori H., M. Gamoto M., Ando T., Matawa K., Hamada M., Hayashi M., Hosokawa S., Hond T., Aoki H., Arita K., Hamada M., Harada C., Aoki H., Arita K., Hamada M., Harada C., An Itoh S., Itoh T., Itoh Y., Itoh Y., Itoh W., Kaniya K., Kanasawa W., Katagiri S., Kikuta A., Kobayashi N., Kono I., Matai Y., Matain T., Mizuno H., Mizubayashi T., Mikai Y., Namasaki H., Nakashima M., Nakama Y., Nakamichi Y., Namagata H., Yoshiki S., Yoshihara R., Yukawa K., Yano M., Jiang J., Gojobai T., Itoh H., Hahn J.H., Kim H.I., Bun M.Y.,
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                                                                                                                                                        anopheles g
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listeria in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oryza sativa (japonica cultivar-group).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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090x67
020984
089819
089818
092d10
0722h3
088723
08872
079881
07079841
0707186
065m55
0733181
081820
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Nature 420:312-316(2002).
EMBL; AP003791; BAB90532.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 29; DB 2; Length 72; 100.0%; Pred. No. 18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      72 AA; 7677 MW; 6A9368D674BE00A3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                      72 AA.
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                                                                                                                                                                                                                                                                                                                     ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
                                       Q8SHP4
Q8Y918
Q92DT0
Q722H3
Q88SK2
Q088SK2
Q7Q8W1
Q7QUG
Q65M5
Q63SIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
01-OCT-2002 (TrEMBLrel. 22,
B1065G12.14 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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TYAMH 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A
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157
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KADA PYRHO
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Matches
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MEDLINE=22022145; PubMed=12024217; DOI=10.1038/417459a;

MEDLINE=22022145; PubMed=12024217; DOI=10.1038/417459a;

MA Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,

Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,

Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.B.A.,

Alves L.M.C., Carnavan F., Cardozo J., Chambergo F., Ciaphna L.P.,

Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,

Ratia J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,

Ratiavama A.M., Kishi L.T., Leite R.P., Lemos B.G.M., Lemos M.V.F.,

Noreira L.M., Novo M.T.M., Menck C.F.M., Miyaki C.Y., Moon D.H.,

Moreira L.M., Novo M.T.M., Okura V.K., Oliveira W.C., Oliveira V.R.,

Pereira H.A., Rossi A., Sana J.A.D., Silva C., Teixeira R.C., Texza R.I.D.,

Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,

Setubal J.C., Kitajima J.P.;

RT "Comparison of the genomes of two Xanthomonas pathogens with differing

Nor Truffi D., Tsai S.M., Whote S.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                            SEQUENCE.
MEDLINE=74175307; PubMed=4208843;
Florent G., Lehman D., Putnam F.W.;
Florent G., Lehman D., Putnam F.W.;
Florent G., Lehman D., Putnam F.W.;
Blochemistry 13:2482-2498(1974).
-! MISCELLANEOUS: This chain was isolated from a Waldenstrom's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                     Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Xanthomonas axonopodis (pv. citri).
Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
Xanthomonadaceae; Xanthomonas.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ig-like.
Pyrrolidone carboxylic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                              macroglobulin.
-- SIMILARITY: Contains 1 immunoglobulin-like domain.
HISP, A00102, 2PB4.
GO: GO: 0005576; C: extracellular; NAS.
GO: GO: 0005878; P: entrigen binding; NAS.
GO: GO: 0008952; P: immune response; NAS.
InterPro; IPR007110; Ig-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    122 122
122 AA; 13166 MW; 74E5B6959E84100A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00406; IGv; 1.
PROSTTE; PS50815; IG LIKE; 1.
Direct protein sequencing; Immunoglobulin V region;
Pyrrolidone carboxylic acid.
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2002 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein XAC2050.
OrderedLocusNames=XAC2050;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT; 158 AA
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1es 5; Conservative
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sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31 TYAMH 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 TYAMH 5
                                                 Mammalia, Euther
NCBI_TaxID=9606;
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Best Local S:
Matches 5
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QBPKV7;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kawarabayaai Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
Yamanoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
Masuchi Y., Shizuya H., Kikuchi H.;
"Complete sequence and gene organization of the genome of a hyper-
thermophilic archaebacterium, Pyrococcus horikoshii OT3.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Archaea; Buryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA Ref. 5:55-76(1998).
-1- CATALYTIC ACTIVITY: ATP + AMP = 2 ADP.
-1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-1- SIMILARITY: Belongs to the archaeal adenylate kinase family.
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                                                                                                                                                                                                 100.0%; Score 29; DB 2; Length 158; 100.0%; Pred. No. 42; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Adenylate kinase (EC 2.7.4.3) (ATP-AMP transphosphorylase)
Name=adkA, OrderedLocusNames=PH1753;
Pyrococcus horikoshii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  196 AA; 22413 MW; 26C834A1BE944D5F CRC64;
                                                                                                                                   158 AA; 17289 MW; CIBIFB23AA6E930B CRC64;
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HSSP; P43410; IKI9.

HAMAP; MF 00234; -; 1.

ATP-binding; Complete proteome; Kinase; Transferase.

ATP-binding; Complete proteome; Konese; Transferase.

SEQUENCE 196 AA; 22413 MW; 26CB34A1BE944D5F CRC64
EMBL; AE011840; AAM36912.1; -.
InterPro; IPR001412; tRNA-synt I.
PR051TE; PS001178; AA_TRNA_LIGAŠE_I; UNKNOWN_I.
COMDLETE POCCEOME.
SEQUENCE 158 AA; 17289 MW; CIBIFB23AA6E930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         196 AA
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Best Local Similarity 100...
Best Local Si Conservative
                                                                                                                                                                                                                                                                   5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                   132 TYAMH 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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Best Local Similarity
Matches 5; Conserv
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                                                                                                                                                                              1 TYAMH 5
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MEDLINE-21349804; PubMed=11456446; DOI=10.1006/dbio.2001.0299;
WADIZENS, Spring JJ, Schmidli C., Schmid V.;
"Conservation of Hox/ParaHox-related genes in the early development of
                                                                                                                                                                                                                                                              STRAIN=ATCC 15692 / PAO1;
STRAIN=ATCC 15692 / PAO1;
STRAIN=ATCC 15692 / PAO1;
STRAIN=2043737; Pubmed=10984043; DOI=10.1038/35023079;
Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Garber R.L., Goltry L., Tolentino E., Weetbrook-Wadman S., Yuan Y., Brody L.L., Spencer D.H., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
"Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathogen.";
Nature 406:959-964(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GO; GO:0005634; C:nucleus; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:00003700; F:transcription of transcription, DNA-dependent; IEA.
InterPro; IPR001356; Homeobox.
InterPro; IPR009057; Homeodomain_11ke.
InterPro; IPR009047; HTH_lambrepressr.
PF000046; Homeobox; 1.
                                                                                                                                                         Pseudomonas aeruginosa.
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transcription factor Cnox4-Pc.
Podocoryne carnea.
Eukaryota, Metazoa, Cnidaria, Hydrozoa, Hydroida, Anthomedusae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; B83290; B83290.
InterPro; IPR002781; DUF81.
Pfam; PF01925; DUF81; Hypothetical protein.
Complete proteome; Hypothetical protein.
SEQUENCE 249 AA; 25989 MW; 8B24827650F64D6A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                  01-MAR-2001 (TrEMBLrel. 16, Last sequence update) 01-JUN-2003 (TrEMBLrel. 24, Last annotation update) Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dev. Biol. 236:89-98(2001).
1- SUBCELLULAR LOCATION: Nuclear (By similarity).
EMBL; AVO36893; AAK63185.1;
HSSP; P09089; IKZ2.
249 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT; 356 AA
                                               Created)
  PRT;
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PROSITE; PS00027; HOMEOBOX_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE004711; AAG06235.1; -.
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PRINTS; PR00031; HTHREPRESSR.
                                            (TrEMBLrel. 16,
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NCBI_TaxID=6096;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 10v...
                                                                                                                                 OrderedLocusNames=PA2847;
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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                                                                                                                                                                                                                                NCBI_TaxID=287;
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                                            01-MAR-2001
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                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                   TISSUE=Human esophagus tumor;
The German Human cDNA Consortium;
Mambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                            100.0%; Score 29; DB 2; Length 356; 100.0%; Pred. No. 97; cive 0; Mismatches 0; Indels
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Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BK640619; CAE45773.1; -.
HSSP; P01861; 1ADQ.
PROSITE; PS50071; HOMEOBOX 2; 1.
DNA-binding; Homeobox; Nuclear protein.
SEQUENCE 356 AA; 41170 MW; EAF5E2308D76C6BB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein-
SEOUENCE 481 AA; 52759 MW; 47220D9E64BDF98B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical protein DKFZp686E23209 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 29; DB 2; L
100.0%; Pred. No. 1.3e+02;
tive 0; Mismatches 0;
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InterPro; IPR003599; Ig.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003596; Ig_W.
Pfam; PF07654; C1-8et; 3.
SWART; SW00400; IG; 2.
SWART; SW00400; IG; 1.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; UNKNOWN_2.
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                                                         Query Match
Best Local Similarity lu...
S; Conservative
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MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185; Adams M.D., Celniker S.B., Holt R.A., Evans C.A., Gocayne J.D., Adams M.D., Celniker S.B., Holt R.A., Evans C.A., Galle R.F., Amanatides P.G., Scherer S.E., Holf R.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brand O., No. Feiffer B.D., M. R. M., Bazer E.G., Helt G., Nelson C.R., Gabor G.L., Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D., Ballew R.M., Bane A., Baxendale J., Bayaktaroglu L., Beasley E.M., Beson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., Autis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I., Autis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I., Abrits K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I., Abrits K.C., Busam D.A., Buller H., Dushor B., Davies P., Abolson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W., Rosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., Abrils M., Goog F., Gorrell J.H., Gu Z., Guan P., Harris M.,
                                                                                                                                                                                                                                                               Rabus R., Ruepp A., Frickey T., Rattei T., Fartmann B., Stark M., Bauer M., Zibat A., Lombardot T., Becker I., Amann J., Gellner K., Teeling H., Leuschner W.D., Gloeckner F.-O., Lupas A.N., Amann R., Klenk H.-P., "The genome of Desulfotalea psychrophila, a sulfate-reducing bacterium
                    Probable acetyl-coenzyme A synthetase.
Name=acs, OrderedLocusNames=DP0825;
Desulfotalea psychrophila.
Bacteria; Proteobacteria; Deltaproteobacteria; Desulfobacterales;
Desulfobulbaceae; Desulfotalea.
                                                                                                                                                                                                                                                                                                                                                                                   from permanently cold Arctic sediments.";
Environ. Microbiol. 6:887-902(2004).
-!- SIMILARITY: Belongs to the ATP-dependent AMP-binding enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-2000 (TrEMBLrel. 13, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
CG3915-PB (GH270399)
Name=Drl-2; ORFNames=CG3915;
Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 29; DB 2; Length 54 llarity 100.0%; Pred. No. 1.5e+02; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 544 AA; 60412 MW; CAD62D99E4CCEBF7 CRC64;
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL, CRE52870; CAG35554.1; -.
GO; GO:0003824; F:catalytic activity; IEA
GO; GO:0008152; P:metabolism; IEA.
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PROSITE; PS00455; AMP_BINDING; 1.
Complete protecome.
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Pfam; PF00501; AMP-binding; 1.
                                                                                                                                                                                                               STRAIN=LSv54 / DSM 12343;
PubMed=15305914;
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les 5; Conserv
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                                                                                                                                                                                             SEQUENCE FROM N.A.
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               The German cDNA CORSOTTIUM;

Bloecker H, Beacher M, Brandt P., Mewes H.W., Weil B., Amid C.,

Bloecker H, Boecher M, Brandt P., Mewes H.W., Weil B., Amid C.,

L Bloecker H, Boecher M, Brandt B.; Amid C.,

L Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.

E MBL: CR749861; CAH18705.1; -.

R EMBL: CR749861; CAH18705.1; -.

R InterPro; IPR001599; Ig. C1.

R InterPro; IPR001599; Ig. C1.

R InterPro; IPR001596; Ig. MHC.

R InterPro; IPR001596; Ig. A.

R Pfam; PF07647; ig; 4.

R Pfam; PF07647; ig; 4.

R SMART; SM00409; IGc; 2.

SMART; SM00406; IG. II.KE; 4.

R PROSITE; PS08085; IG LIKE; 4.

R PROSITE; PS08085; IG LIKE; 4.

R PROSITE; PS08085; IG. MHC; UNKNOWN_2.
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Enterobacteriaceae; Escherichia.
NCBI_TaxID=562;
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SIGNIENCE FROM N.A.
SIGNIENCE R.C., Delicato E.R., Gaziri L.C.J., Vidotto M.C.;
Submitted (AFR-2003) to the EMBL/GenBank/DDBJ databases.
Submitted (AFR-2003) to the EMBL/GenBank/DDBJ databases.
R EMBL, A7280856, AAP13781.1; -.
R GO; GO:0004252; F:serine-type endopeptidase activity; IEA.
R GO; GO:0006508; P:proteclysis and peptidolysis; IEA.
R InterPro; IPR0090710; Peptidase S6.
R InterPro; IPR009003; Pept_Ser_Cys.
R Pfam; PF02395; IGAl; 1.
R PRINTS; PR00921; IGASERPTASE.
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Local Similarity 100.0%; Pred. No. 1.5e+02;
nes 5; Conservative 0; Mismatches 0; Indels
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01-UTN-2003 (TrEMBLrel. 24, Last sequence update)
01-UNAR-2004 (TrEMBLrel. 26, Last annotation update)
Tsh protein (Fragment).
Escherichia coli.
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Q6AQ19;
25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
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Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein
TISSUE=Rectum tumor;
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SEQUENCE
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RESULT 10 Q6AQ19 ID Q6AQ19 AC Q6AQ19 DT 25-OC7

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           Hostin D., Houston K.A., Howland T.J., Mei M.H., Ibegwam C., Jalali M., Kalush P., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Lasi Z., Lasko D., Lei Y., Li Z., Liang Y., Lin Z., Liang Y., Lin X., Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., McKulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., Palazzolo M., Pitteman G.S., Pan S., Pollard J., Puri V., Resee M.G., Reinert K., Remington K.A., Nixon K., Suuskern D.R., Pacleb J.M., Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Spralling A.C., Turner R., Venter B., Wang A.H., Wang X., Wassarman D.A., Weinstock G.M., Weissenbach J., Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Yen R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zhan G., Zhu S., Zhu X., Zhu S., Zhu X., Zhu S., Zhu Z., Z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=21426065; PubMed=12537568;
MEDLINE=22426065; PubMed=12537568;
MEDLINE=21426065; PubMed=12537568;
MEDLINE=21426065; PubMed=12537568;
Medliker S.E., Wheeler D.A., Krommiller B., Frise B., Hodgson A.,
Patel S., Adams M., Champe M., Dugan S.P., Frise B., Hodgson A.,
George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
Patelb J.M., Park S., Feiffer B.D., Richards S., Sodergren B.J.,
Weinskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
Weinstock G., Scherer S.E., Myers E.W., Glbbs R.A., Rubin G.M.;
Meinstock G., Scherer S.E., Myers E.W., Glbbs R.A., Rubin G.M.;
melanogaster euchromatic genome sequence.";
Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
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Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R., Fatel S., Frise E., Meeler D.A., Lewis S.E., Rubin G.M., Ashburner M., Celniker S.E.;
"The transposable elements of the Drosophila melanogaster euchromatin:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE=22426069; PubMed=12537572;
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Misra S., Crosby M.A., Mungall C.J., Millburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman B.P.,
Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
Harris N.L., Richter J., Kusso S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=Berkeley;
Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Chaque M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,
Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S.,
Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lewis S.E.; "Annotation of the Drosophila melanogaster euchromatic genome: a
  Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           a genomics perspective.";
Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      systematic review.";
Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
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Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
NCBI TaxID=5062;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 648;
                                 HSSP, P08581, IRIW.
FlyBase, FB9003791; Drl-2.
GO, GO:000524; F:ATP binding; IEA.
GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
GO; GO:0004740; F:transferase activity; IEA.
GO; GO:0016468; P:protein amino acid phosphorylation; IEA.
InterPro; IPR010719; Prot_Kinase.
InterPro; IPR00719; Prot_Kinase.
InterPro; IPR001266; Tyr_pkinase.
InterPro; IPR003306; MF.
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Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
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SEQUENCE 648 AA; 71139 MW; 1B4FAA60CB84E457 CRC64;
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ol-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Glutaminase (EC 3.5.1.2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 29; DB 2; I
100.0%; Pred. No. 1.8e+02;
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PRINTS; PR00109; TYRKINASE.

ProDom; PP000001; Prot Kinase; 1.

PROSITE; PS00119; PROTEIN KINASE DOM; 1.

PROSITE; PS00109; PROTEIN KINASE TYR; UNKNOWN 1.

PROSITE; PS50814; WIF; 1.
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GO; GO:0004359; F:glutaminase activity; IEA.
GO; GO:0016787; F:hydrolase activity; IEA.
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EMBL; AE003820; AAF58429.3; -. EMBL; BT004493; AAO42657.1; -.
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Best Local Similarity 100.0%;
Matches 5; Conservative C
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les 5; Conserv
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Glutaminase
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01-MAY-2000
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                                                                                                                                                          MEDLINE=20406523; PubMed=10952006;
Koibuchi K., Nagasaki H., Yuasa A., Kataoka J., Kitamoto K.;
Koibuchi K., Nagasaki H., Yuasa A., Kataoka J., Kitamoto K.;
"Molecular cloning and characterization of a gene encoding glutaminase
from Aspergillus oryzae.";
Appl. Microbiol. Biotechnol. 54:59-68(2000).
EMBL, AB029552; BAA86534.1;
SEQUENCE 690 AA; 76164 MW; E3D0B17841EEA00D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                             Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
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Afonso C.L., Tulman E.R., Lu Z., Zsak L., Kutish G.F., Rock D.L.;
"The genome of fowlpox virus.";
"The Janone of fowlpox virus.";
J. Virol. 74:3815-3831(2000).
-i- SIMILARITY: Contains 14 ANK repeats.
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Aspergillus oryzae.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
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16-0CT-2001 (Rel. 40, Last sequence update)
05-JUU-2004 (Rel. 44, Last annotation update)
Putative ankyrin-repeat protein FPV222.
Name=FPV222;
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INEEPPO; IPR002110; ANK.
INTEEPPO; IPR002110; R-box.
Pfam; PF00646; F-box.
Pfam; PF00464; F-box.
PRMTS; SM0248; ANKYRIN.
SMART; SM0248; ANKYRIN.
PROSITE; PSS0297; ANK REP REGION; 1.
PROSITE; PSS0297; ANK REP REGION; 1.
ANK repeat; Hypothetical protein; Repeat.
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NCBI_TaxID=10261;
                                                              NCBI_TaxID=5062;
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MEDLINE=98332770; PubMed=9665876; DOI=10.1126/science.281.5375.375;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Treponema pallidum.
Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
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                                                                                                                                                                                                    100.0%; Score 29; DB 1; Length 747; 100.0%; Pred. No. 2.1e+02;
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Complete proteome; Hypothetical protein.
SEQUENCE 1151 AA; 127556 MW; EDB6353C32CB4056 CRC64;
                                                                                                                                                                                                                                                    Indels
                                                                                                                                                85303 MW; 55F90AF2855C3D28 CRC64;
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25-OCT-2004 (Rel. 45, Last annotation update)
Hypothetical protein TP0245.
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Science 281:375-388(1998).
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Sequence 45, Appl
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Sequence 7091, Appl
Sequence 21, Appl
Sequence 26, Appl
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Sequence 26, Appl
Sequence 11, Appl
Sequence 26, Appl
Sequence 21, Appl
Sequence 10, Appl
Sequence 11, Appl
Sequence 26, Appl
Sequence 11, Appl
Sequence 12, Appl
Sequence 13, Appl
Sequence 11, Appl
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                                                                                                                                     October 14, 2005, 16:00:04; Search time 9.84375 Seconds (without alignments) 37.917 Million cell updates/sec
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/cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
                   GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd
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US-09-232-290-45
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US-10-262-991A-26228
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US-09-270-767-35497
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US-09-949-016-5992
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US-09-919-038-270
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US-09-318-667-21
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US-09-138-091A-26
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US-09-424-840B-91
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Maximum Match 100%
Listing first 45 summaries
                                                                                                       - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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US-09-23-290-45

Sequence 45, Application US/09232290A

Sequence 45, Application US/09232290A

Patent No. 6815540

GENERAL INFORMATION:

APPLICANT: HUNEGGER, ANNEMARIE

TITLE OF INVENTION: IMMONGCLOBULIN SUPER FAMILY DOMAINS AND FRAGMENTS WITH

TITLE OF INVENTION: INCREASED SOLUBILITY

FILE REPRESENCE: MORRHO/7

CURRENT APPLICATION NUMBER: US/09/232, 290A

CURRENT APPLICATION NUMBER: US/09/232, 290A

CURRENT APPLICATION NUMBER: CT/EP96/02230
24, Appl
24, Appl
24, Appl
24, Appl
143, Appl
10, Appl
11, Appl
46, Appl
46, Appl
46, Appl
46, Appl
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APPLICANT: Admentation:
APPLICANT: Baron, Dan L.
APPLICANT: Baron, Dan L.
APPLICANT: Hase, Philip E.
APPLICANT: Gudget, Paniel
APPLICANT: Suggett, Shelley
TITLE OF INVENTION: Human Anti-Factor IX/IXa Antibodies
TITLE OF INVENTION: Human Anti-Factor IX/IXa Antibodies
TITLE OF INVENTION: Human Anti-Factor IX/IXa Antibodies
CURRENT APPLICATION NUMBER: US/09/383,667
CURRENT FILING DATE: 1999-08-26
EARLIER FILING DATE: 1999-08-26
EARLIER PEPLICATION NUMBER: US 60/098,233
EARLIER FILING DATE: 1999-03-03
EARLIER PELLING DATE: 1999-03-03
NUMBER OF SEQ ID NOS: 32
SEQ ID NO 10
ILENGTH: S
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US-02-248-76A-14399
US-08-331-398A-46
US-08-561-521-12
US-08-561-521-12
US-08-561-521-13
US-08-331-397B-46
US-08-227-633-46
US-09-227-633-46
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100.0%; Pred. No. 4.1e+05;
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PCT-US95-01219-12
PCT-US95-01219-13
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Patent No. 6624295
GENERAL INFORMATION:
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; ORGANISM: Homo sapiens
US-09-383-667-10
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Best Local Similarity
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TYAMH 5
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Sequence 18, Application US/10262083

Patent No. 6830905

Patent No. 6830905

APPLICANT: NORMATION:
APPLICANT: WAGASAKI, Hiroaki
APPLICANT: KATAOKA, Jiro
APPLICANT: WANGA, Jiro
APPLICANT: WANGA, Jiro
CURRENT PILING DATE: 199438US-8222-10-0-PCT
CURRENT FILING DATE: 2002-10-02
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Patent No. 6703491

GENERAL INFORMATION

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERRNCE: File Reference: 7326-094

CURRENT FILLING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517
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100.0%; Pred. No. 1.1e+02;
ative 0; Mismatches 0;
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PRIOR FILING DATE: 2000-11-15

PRIOR APPLICATION NUMBER: US/09/674,507

PRIOR APPLICATION NUMBER: UP 10/134080

PRIOR PILING DATE: 1998-05-15

PRIOR PILING DATE: 1998-09-11

PRIOR PILING DATE: 1998-10-14

PRIOR PILING DATE: 1998-10-14

PRIOR PILING DATE: 1999-10-14

PRIOR PILING DATE: 1999-10-14

PRIOR PILING DATE: 1999-05-12

NUMBER OF SEQ ID NOS: 26

SEQ ID NO 18

LENGTH: 690
PRIOR APPLICATION NUMBER: PCT/JP99/02455
PRIOR FILING DATE: 1999-05-12
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
LENGTH: 690
                                                                                                                                                                 , ORGANISM: Aspergillus oryzae
US-10-262-083-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Aspergillus oryzae US-10-262-083-18
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Best Local Similarity 100.
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Best Local Similarity
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                                                                                                                                           TYPE: PRT
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Sequence (26228, Application US/09252991A)

Patent No. 6551795

GENERAL INFORMATION:

HITLE OF INVENTION:

TITLE OF INVENTION:

ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION:

TITLE OF INVENTION:

ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE:

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT PILING DATE: 1999-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 26228

LENGTH: 258
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Patent No. 6830905
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: KOIBUCHI, Kyoko
APPLICANT: VUASA, Ari
APPLICANT: KATAOKA, Airoaki
APPLICANT: KATAOKA, Aisouhiko
TITLE OF INVENTION: A No. 6830905el Glutaminase, its Gene and a Method of Producing
FILE REPERENCE: 199438US-8222-10-0-PCT
CURRENT APPLICATION NUMBER: US/10/262,083
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PRIOR FILING DATE: 2000-11-15
PRIOR PELICATION NUMBER: US/09/674,507
PRIOR PELICATION NUMBER: JP 10/134080
PRIOR PELICATION NUMBER: JP 10/258974
PRIOR PELICATION NUMBER: JP 10/292443
PRIOR FILING DATE: 1998-09-11
PRIOR PELICATION NUMBER: JP 10/292443
PRIOR PELICATION NUMBER: JP 11/89157
PRIOR PELICATION NUMBER: JP 11/89157
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CRGANISM: Pseudomonas aeruginosa
US-09-252-991A-26228
EARLIER FILING DATE: 1996-05-23
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 45
LENGTH: 118
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Best Local Similarity 100.v
Laca 5; Conservative
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Best Local Similarity 100.
Matches 5; Conservative
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                                                                                                                TYPE: PRT
ORGANISM: Murine
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MS-09-543-681A-8288

Sequence 8288, Application US/09543681A

Sequence 8288, Application US/09543681A

Sequence 8288, Application US/09543681A

Sequence 8288, Application US/09543681A

GENERAL INFORMATION:
TITLE OF INVENTION: ULACADIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL
TITLE OF INVENTION: UNMBER: US/09/543,681A

CURRENT PILING DATE: 2000-04-05

PRIOR APPLICATION NUMBER: US 60/128,706

PRIOR PILING DATE: 1999-04-09

NUMBER OF SEQ ID NOS: 8344

SEQ ID NO 8288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence 5992, Application US/09949016

patent No. 681239

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
FILE REPRENEUE: CLOOKINOT
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
FRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
SPRIOR FILING DATE: 2000-10-03
SPRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
SPRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
SPRIOR FILING DATE: 2000-10-03
PRIOR SPRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
SOUTHARE: FREEEER FASTER FOR WINDOWS VERSION 4.0
SEQ ID NO 5992
LENGHH: 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 26; DB 4; Length 455; Pred. No. 3.6e+02; 1; Mismatches 0; Indels
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; Sequence 7091, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 26; DB 4; Length 502
Pred. No. 3.9e+02;
1; Mismatches 0; Indels
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Best Local Similarity 80.0%;
Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-8288
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Best Local Similarity 80.0
Matches 4; Conservative
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398 TYALH 402
  152 TYALH 156
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US-09-949-016-5992
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US-09-949-016-5992
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Facett No. 6610836;
GENERAL INFORMATION:
TITLE OF INVENTION: Breton et. al
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFRENCE: 2709.2004001
CURRENT FILING DATE: 2000-01-27
FRICK REPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 1999-01-29
FRICK FILING DATE: 1999-01-29
SEQ ID NO 10284
LENGTH: 454
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US-09-270-767-50714

US-09-270-767-50714

Patent No. 6703491

GENERAL INFORMATION:

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster

FILE REFERENCE: File Reference: 7326-094

CURRENT PAPLICATION NUMBER: US/09/270,767

UNWBER OF SEQ ID NOS: 62517

SOFTWARE: PatentIn Ver. 2.0

LENGTH: 108

LENGTH: 108
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                                                                                                                                                                                       Score 26; DB 4; Length 108;
Pred. No. 85;
1; Mismatches 0; Indels
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Pred. No. 85;
1; Mismatches 0; Indels
                                                                                                                           ; OTHER INFORMATION: Xaa means any amino acid US-09-270-767-35497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Xaa means any amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Drosophila melanogaster
                                                             TYPE: PRT
ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                       89.7%;
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 35497
LENGTH: 108
                                                                                                                                                                     Query Match
Best Local Similarity 80.v-
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Best Local Similarity 80.v
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Best Local Similarity 80.0
Matches 4; Conservative
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TYALH 68
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US-09-489-039A-10284
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                                                                                                          FEATURE:
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Fatent No. 5639863
GENERAL INFORMATION:
APPLICANT: Michael D. Dan
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES SPECIFIC TO
TITLE OF INVENTION: CELL CYCLE-INDEPENDENT GLIOMA SURFACE
TITLE OF INVENTION: ANTIGEN
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEER: Ridout & Maybee
STREET: 2300 Richmond-Adelaide Centre
STREET: 101 Richmond Street West
                                                                                                                                                                                                                                 Length 544;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 86.2%; Score 25; DB 1; Length 5; Best Local Similarity 80.0%; Pred. No. 4.1e+05; Matches 4; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                          0; Indels
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                                                                                                                                        ; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. 6727066 4113161CD1
US-09-919-039-270
                                                                                                                                                                                                                            89.7%; Score 26; DB 4; I
80.0%; Pred. No. 4.3e+02;
tive 1; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 536
PRIOR APPLICATION DATA: No. 5639863 applic.
ATTORNEY/ACENT INFORMATION:
NAME: Lake, James R.
REGISTRATION NUMBER: 31081
REFERENCE/DOCKET NUMBER: NOVOP/106A/7551
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC Compatible OPERATING SYSTEM: MS-DOS 6.00 SOFTWARE: ASCII Editor CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/264,093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: not applicable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (416) 868-11482
TELEFAX: (416) 362-0823
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                            Query Match
Best Local Similarity 80.v-
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         SOFTWARE: PERL Program
SEQ ID NO 270
LENGTH: 544
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TOPOLOGY: linear
US-08-264-093-21
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ZIP: M5H 2J7
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US-08-918-148-26
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APPLICANT: Furness, Michael
APPLICANT: Furness, Michael
APPLICANT: Buchbinder, Jenny
TILE REPERENCE: DOINVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS FILE REPERENCE: PA-0041 US
CURRENT APPLICATION NUMBER: US/09/976,594
CURRENT FILING DATE: 2000-10-12
PRIOR PILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 1143
SEQ THANKE: PERL PROGRAM
SEQ ID NO 699
LENGTH: 544
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARES: PASISEQ for Windows Version 4.0
SEQ ID NO 7091
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Sequence 270, Application US/09919039
Patent No. 6727066
GENERAL INFORMATION:
APPLICANT: KASET, MATTHEW R.
APPLICANT: KASET, MATTHEW R.
TILLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES FILE REFERENCE: PA.0035 US
CURRENT APPLICATION NUMBER: US/09/919,039
CURRENT FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: 60/222,113
PRIOR APPLICATION NUMBER: 60/222,113
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 401
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Pred. No. 4e+02;
1; Mismatches 0; Indels
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OTHER INFORMATION: Incyte ID No. 6673549 4113161CD1
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Best Local Similarity 80.0
Matches 4; Conservative
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403 TYALH 407
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                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                              US-09-949-016-7091
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US-09-976-594-699
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; Sequence 26, Application US/08918148A
; Patent No. 634220
; GENERAL INPORMATION:
; APPLICANT: Adams, Camellia
; APPLICANT: Gurrer, Paul J.
; APPLICANT: Gurrer, Paul J.
; APPLICANT: Gurrer, Paul J.
; APPLICANT: Gurrer, Austin L.
; TITLE OF INVENTION: Agonist Antibodies
; CURRENT FILING DATE: 1997-08-25
; CURRENT FILING DATE: 1997-08-25
; NUMBER OF SEQ ID NOS: 79
; SEQ ID NO 26
LENGTH: 5
; TYPE: PRT
; NAME, KEY: 1010 ScFV, 1285 ScFV VH CDR1
; COCANION: 1-5
; OTHER INFORMATION:
; COCATION: 1-5
; OTHER INFORMATION:
US-08-918-148-26

Query Match
Best Local Similarity 80.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Qp
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Search completed: October 14, 2005, 16:22:00 Job time : 10.8438 secs

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 34, Appl
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                                                                                                                October 14, 2005, 16:20:10; Search time 35.5469 Seconds (without alignments) 58.615 Million cell updates/sec
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1: \cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: \cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: \cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
4: \cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
5: \cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
6: \cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
6: \cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
7: \cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
9: \cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
10: \cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
11: \cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
11: \cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
11: \cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
12: \cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
13: \cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
14: \cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
15: \cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
16: \cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
17: \cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
18: \cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
19: \cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
21: \cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
22: \cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
                                                                                                                                                                                                                                                                                                                                                                                    1859788
GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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US-11-0468-543-91
US-11-003-819-12
US-10-66-242-25
US-10-989-462-7
US-10-466-242-47
US-10-466-242-47
US-10-466-242-47
US-10-46-215-311733
US-10-425-115-311634
US-10-282-122A-52731
US-10-989-462-34
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                                                                                                                                                                                                                                                                                                                                          1859788 seqs, 416717961 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                            OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                              BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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29
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Match Length
                Copyright
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Perfect score:
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ALIGNMENTS

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GENUERAL INFORMATION US/10989462

| Sequence 64, Application US/10989462
| Sequence 64, Application US/10989462
| Sequence 64, Application No. US20050220795A1
| GENERAL INFORMATION: The Company of the
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sequence 25, Application US/10466242
Publication No. US20040208887A1
GENERAL INFORMATION:
APPLICANT: Drakenberg, Katarina
APPLICANT: Drakenberg, Katarina
TITLE OF INVENTION: Materials and methods for treatment of hepatitis C
FILE REFERENCE: 0380-P032480500;
CURRENT APPLICATION NUMBER: US/10/466,242
CURRENT FILING DATE: 2004-01-16
PRIOR APPLICATION NUMBER: PCT/SE02/00044
PRIOR APPLING DATE: 2002-01-14
NUMBER OF SEQ ID NOS: 56
SSO ID NO 25
LENGTH: 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT WILTUD, K. Dane
APPLICANT WILTUD, K. Dane
TITLE OF INVENTION: ANTI-HYDROXYLASE ANTIBODIES AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 01997-329001
CURRENT APPLICATION NUMBER: US/10/989,462
CURRENT FILING DATE: 2004-11-15
PRIOR APPLICATION NUMBER: US 60/520,114
PRIOR PILING DATE: 2003-11-14
PRIOR FILING DATE: 2003-11-14
PRIOR FILING DATE: 2003-11-14
SPIOR FILING DATE: 2003-10-14
SPIOR FILING DATE: 2004-04-19
SPIOR FILING DATE: 2004-04-19
SPIOR FILING DATE: 2004-04-19
SPIOR FILING DATE: 2004-04-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; LOCATION: (1)..(121)
; OTHER INFORMATION: Clone 2a:14 VH
US-10-466-242-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 7, Application US/10989462; Publication No. US20050220795A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: Artificial Sequence
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Best Local Similarity 100...
Page 5; Conservative
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Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
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                                                                US-10-468-543-91
; Sequence 91, Application US/10468543
; Sequence 91, Application US/10468543
; Publication No. US20040091938A1
; GENERAL INFORMATION:
; APPLICANT: Irimura, Tatsuro
; APPLICANT: Mateumoto, Mariko
; APPLICANT: Wim, Mijuug
; APPLICANT: Wim, Mijuug
; APPLICANT: Wim, Mijuug
; PILE NEFERRNCE: 03-786
; CURRENT APPLICATION NUMBER: US/10/468,543
; CURRENT APPLICATION NUMBER: US/10/468,543
; CURRENT FILING DATE: 2003-08-20
; PRIOR PILING DATE: 2001-02-20
; PRIOR FILING DATE: 2001-02-20
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: PatentIn version 3.1
; ENGTHALE: 11
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| Bublication No. US2005015832A1
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| APPLICANT: Evans, Elizabeth E. |
| APPLICANT: Sahasrabudhe, Deepak M. |
| APPLICANT: Sahasrabudhe, Deepak M. |
| APPLICANT: Satuderer, Maurice |
| FILE OF INVENTION: Exposed on Apoptotic Tumor Cells |
| FILE REFERENCE: 1843.019002 |
| CURRENT APPLICATION NUMBER: US/11/003,819 |
| CURRENT PILING DATE: 2003-12-04 |
| PRIOR APPLICATION NUMBER: US 60/531,688 |
| PRIOR PILING DATE: 2003-12-23 |
| NUMBER OF SEQ ID NOS: 61 |
| SEQ ID NO 12 |
| LENGTH |
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US-10-468-543-91
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Best Local Similarity 100.1
Then 5; Conservative
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US-11-003-819-12
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ORGANISM: Artificial
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Sequence 211694, Application US/10425115

Fublication No. US20040214272A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: 191ants
TITLE OF INVENTION: US-105222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT PILING DATE: 2003-64-28
NUMBER OF SEQ ID NOS: 369326

SEQ ID NO 211694

LENGTH 158
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US-10-424-599-231272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Clone ID: MRT4577_124664C.1.pep
US-10-425-115-211694
                                                                              TYPE: PRT
ORGANISM: Glycine max
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(151)
OTHER: INFORMATION: unsure at all Xaa locations
FEATURE:
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OTHER INFORMATION: unsure at all Xaa locations
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                                                                                                                                                                                                                                                                                                                                     0; Mismatches
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CURRENT FILING DATE: 2003-04-28 NUMBER OF SEQ ID NOS: 285684 SEQ ID NO 231272 LENGTH: 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zyskind, Judith
Wall, Daniel
Trawick, John
                                                                                                                                                                                                                                                                                                               Local Similarity 100.
nes 5; Conservative
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Carr, Grant
                                                                                                                                                                                                                                                                                                                                                                                                                        120 TYAMH 124
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ORGANISM: Zea mays
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NAME/KEY: unsure
LOCATION: (1)..(1
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APPLICANT:
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Matches
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US-10-45-115-311733, Application US/10425115

SEQUENCE 311733, Application No. US20040214272A1

GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Cao, Yongwei J.
TITLE OF INVENTION: Wileic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)
CURRENT APPLICATION NUMBER: US/10/425,115

CURRENT PILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 369326

SEQ ID NO 311733

LENGTH: 137
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Sequence 231272, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Thuy Thuy Thuy
APPLICANT: Can Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plante and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21 (53223) B
CURRENT APPLICATION NUMBER: US/10/424,599
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                 TITLE OF INVENTION: Materials and methods for treatment of hepatitis C FILE REPERENCE: 0380-P03248US00
CURRENT APPLICATION NUMBER: US/10/466,242
CURRENT FILING DATE: 2004-01-16
PRIOR APPLICATION NUMBER: PCT/SE02/00044
PRIOR FILING DATE: 2002-01-14
NUMBER OF SEQ ID NOS: 56
SOFTWARE: Patentin version 3.1
SEQ ID NO 47
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                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 29; DB 16; Length 128; 100.0%; Pred. No. 76;
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; OTHER INFORMATION: Clone ID: MRT4577_47353C.1.pep
US-10-425-115-311733
                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
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; OTHER INFORMATION: Clone 2b:5 VH
US-10-466-242-47
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Best Local Similarity 100.
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5; Conservative
    Persson, Mats
                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
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PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR FILING DATE: 2000-05-21

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-05-06

PRIOR FILING DATE: 2000-05-06

PRIOR FILING DATE: 2000-05-06

PRIOR FILING DATE: 2000-05-06

PRIOR PLING DATE: 2000-10-23

PRIOR PLING DATE: 2000-110-23

PRIOR PLING DATE: 2000-110-23

PRIOR PLING DATE: 2000-112-22

PRIOR PLING DATE: 2001-01-27

PRIOR PLING DATE: 2001-02-09

PRIOR PLING DATE: 2001-02-09

PRIOR FILING DATE: 2001-02-09

PRIOR PLING DATE: 2001-02-09

PRIOR PLING DATE: 2001-02-09

PRIOR PLING DATE: 2001-02-09

PRIOR PLING DATE: 2001-02-16

PRIOR PLING DATE: 2001-02-03
                                APPLICANT: Forsyth, R. APPLICANT: Xu, H. TITLE OF INVENTION: 1 dentification of Essential Genes in Microorganisms FILE REFERENCE: ELITRA.034A CURRENT APPLICATION NUMBER US/10/282,122A CURRENT FILING DATE: 2003-02-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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100.0%; Score 29; DB 15; Length 206;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels
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Sequence 34, Application US/10989462;
Publication No. US20050220795A1
GENERAL INFORMATION:
APPLICANT: Wittrup, K. Dane;
APPLICANT: Yeung, Yik Andy
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 01997-329001
CURRENT FILING DATE: 2004-11-15
PRIOR APPLICATION NUMBER: US 60/520,114
PRIOR APPLICATION NUMBER: US 60/520,114
PRIOR FILING DATE: 2003-11-14
PRIOR FILING DATE: 2004-19
NUMBER OF SEQ ID NOS: 319
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 34
ILENGTH: 257
TYBE: PRI
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; OTHER INFORMATION: Synthetically generated peptide
US-10-989-462-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Clostridium botulinum
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Yamamoto, Robert
Forsyth, R.
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Best Local Similarity
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US-10-989-462-34
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Sequence 9985, Application US/10369493
; Sequence 9985, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
    APPLICANT: Hinkle, Gregory J.
    APPLICANT: Hinkle, Gregory J.
    APPLICANT: Goldman, Barry S.
    PRICANT: Goldman, Barry S.
    PRICANT
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APPLICANT: KOIBUCHI, Kyoko
APPLICANT: KOIBUCHI, Kyoko
APPLICANT: WAGASAKI, Hiroaki
APPLICANT: WAGASAKI, Hiroaki
APPLICANT: WAGASAKI, Hiroaki
APPLICANT: WAGASAKI, Hiroaki
APPLICANT: KATANOTO, Katsuhiko
ITITE OF INVENTION: A No. US20030170670alel Glutaminase, its Gene and a Method of Prc
ITITE OF INVENTION: A No. US20030170670alel Glutaminase, its Gene and a Method of Prc
ITITE OF INTERNATE: 19943005-822-10-0-PCT
CURRENT APPLICATION NUMBER: US/10/262,083
CURRENT FILING DATE: 1998-00-11-15
PRIOR FILING DATE: 1998-09-11
PRIOR APPLICATION NUMBER: UP 10/258974
PRIOR PILING DATE: 1998-09-11
PRIOR APPLICATION NUMBER: UP 11/89157
PRIOR PILING DATE: 1998-10-14
PRIOR PILING DATE: 1999-03-30
PRIOR PILING DATE: 1999-05-12
PRIOR APPLICATION NUMBER: PCT/JP99/02455
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US-10-369-493-9985
    Mismatches
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Publication No. US20030170670A1
GENERAL INFORMATION:
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; LENGTH: 690
; TYPE: PRT
; ORGANISM: Aspergillus oryzae
US-10-262-083-2
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Best Local Similarity 100.
         5; Conservative
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US-10-369-493-9985
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Query Match
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels C
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 19 10/256974
PRIOR PILING DATE: 1998-09-11
PRIOR PILING DATE: 1998-09-11
PRIOR PILING DATE: 1998-10-14
PRIOR PILING DATE: 1998-10-14
PRIOR PILING DATE: 1998-10-14
PRIOR PILING DATE: 1999-03-30
PRIOR PILING DATE: 1999-05-12
PRIOR PILING DATE: 1999-05-13
PRIOR PILING DATE: 1999-05-
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; ORGANISM: Aspergillus oryzae
US-10-851-337-2
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Sequence 2, Application US/100551337

Publication No. US20040229322A1

GENERAL INFORMATION:
APPLICANT: KOIBUCHI, Kyoko

APPLICANT: XTAOKA, Ari

APPLICANT: XTAOKA, Ari

APPLICANT: KITAMORO, Kateuhiko

TITLE OF INVENTION: A Novel Glutaminase, its Gene and a Method of

TITLE OF INVENTION: A Novel Glutaminase, its Gene and of

TITLE OF INVENTION: A Novel Glutaminase, its Gene and of

TITLE OF INVENTION: A Novel Glutaminase, its Gene and of

TITLE OF INVENTION: A Novel Glutaminase, its Gene and of

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                                                           Query Match 100.0%; Score 29; DB 14; Length 690; Best Local Similarity 100.0%; Pred. No. 3.9e+02; Matches 5; Conservative 0; Mismatches 0; Indels 0
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CURRENT FILING DATE: 2002-10-02.

PRIOR APPLICATION NUMBER: US/09/674,507

PRIOR PILING DATE: 2000-11-15

PRIOR FILING DATE: 1998-05-15

PRIOR FILING DATE: 1998-05-15

PRIOR FILING DATE: 1998-05-11

PRIOR PRILING DATE: 1998-09-11

PRIOR PILING DATE: 1998-09-11

PRIOR PILING DATE: 1998-09-11

PRIOR PILING DATE: 1998-09-11

PRIOR PILING DATE: 1998-10-14

PRIOR PILING DATE: 1998-03-10

PRIOR PILING DATE: 1998-03-10

PRIOR PILING DATE: 1999-03-10

PRIOR PILING DATE: 1999-03-10
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PRIOR APPLICATION NUMBER: US/10/262,083
PRIOR FILING DATE: 2002-10-02
PRIOR APPLICATION NUMBER: US/09/674,507
PRIOR FILING DATE: 2000-11-15
PRIOR APPLICATION NUMBER: UF 10/134080
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; ORGANISM: Aspergillus oryzae
US-10-262-083-18
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Best Local Similarity 100.
Matches 5; Conservative
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- protein search, using sw model OM protein October 14, 2005, 15:51:19; Search time 130.688 Seconds (without alignments) 50.310 Million cell updates/sec Run on:

US-10-614-959-11 88

1 IISYDGSKKYYADSVKG 17 score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

2105692 segs, 386760381 residues Searched:

Total number of hits satisfying chosen parameters:

2105692

Minimum

seq length: 0 seq length: 200000000 88 Maximum Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqT1980s:* geneseqT0900s:* geneseqT2000s:* geneseqT2001s:* geneseqT2003as:* geneseqT2003as:* A_Geneseq_16Dec04:* •• Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2004s:*

SUMMARIES

	Anti-fact	Anti-IL-4	an BLy		an BLy	Single ch	Single ch	Single ch	an BLy	Single ch	Human het	sHigM22 h	Anti-GPI-	Human ant	BHigM22 h	Human ant	Anti-fact	an ant	an ant	an het	an het	an BLy	Single ch	Human ant	Plasmid s
i O	Ant	Ant	Human	Human	Human	Sin					Hum	BHi	Ant	Hum	BHI	Hum	Ant	Нишап	Human	Human	Human				Pla
Description	Aay79069	Abb07230	Abp45312	Abp44905	Abp44903	Adg95730	Adg95732	Adg96139	Abp45103	Adg95930	Add28319	Abb07186	Abo33850	Abo33836	Abb07169	Adi26654	Aay79076	Adp22108	Ade28443	Add28233	Add28321	Abp45679	Adg96506	Ade28467	Abb06275
£	AAY79069	ABB07230	ABP45312	ABP44905	ABP44903	ADG95730	ADG95732	ADG96139	ABP45103	ADG95930	ADD28319	ABB07186	ABO33850	AB033836	ABB07169	ADI26654	AAY79076	ADP22108	ADE28443	ADD28233	ADD28321	ABP45679	ADG96506	ADE28467	ABB06275
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AAW90298 AAY79074 AAY79078 AAO17790 ADJ32094 ADJ32094 ADJ32094 ADJ32094 ADS52370 ADS52340 ADS52430 ADS52430 ADS52430 ADS52430 ADS52430 ADS6956 ADS6975 AAR76975	ABU56837 ABU56866 AAW62799 AAB40127
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ALIGNMENTS

Complementarity determining region 2; CDR2; antibody; Gla domain; factor IX/IXa; blood coagulation; deep venous thrombosis; arterial thrombosis; unstable angina; post myocardial infarction; coronary artery bypass graft; CABG; stroke; tumour growth; metastasis; percutaneous transluminal coronary angioplasty; PTCA, inflammation; septic shock; hypotension; adult respiratory distress syndrome; ARDS; arterial fibrillation; disseminated intravascular coagulopathy; DIC. Anti-factor IX/IXa antibody H chain V domain CDR2 amino acid sequence. AAY79069 standard; peptide; 17 AA 12-JUN-2000 (first entry) AAY79069;

99WO-US019453. WO200012562-A1. Homo sapiens. 26-AUG-1999; 09-MAR-2000.

98US-0098233P. 99US-0122767P. 28-AUG-1998; 03-MAR-1999;

(GETH) GENENTECH INC.

Devaux B, Eaton DL, Hass PE, Judice JK, Kirchhofer D; Adams CW, Suggett S;

WPI; 2000-256595/22.

Novel human anti-Factor IX/IXa antibodies against IX/IXa gamma-carboxyglutamic acid domains useful as anti-coagulant in thrombosis, stroke, and post myocardial infarction.

Claim 2; Fig 2; 84pp; English.

This sequence represents a complementarity determining region 2 (CDR2) of the heavy chain variable domain of a human anti-factor IX/IXa Gla domain antibody. Factor IXa is a vitamin K dependent plasma serine protease that participates in the blood cogulation pathways. The Gla domain of factor IXa and its zymogen factor IX contains important structural determinants for interaction with high affinity binding sites on vascular endothelial

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the treatment or prophylaxis of thrombotic or coagulopathic diseases or disorders in a mammal for which inhibiting a FIX/IXa mediated event is disorders in a mammal for which inhibiting a FIX/IXa mediated event is indicated, e.g. deep venous thrombosis, arterial thrombosis, unstable angina, post myocardial infarction, post surgical thrombosis, coronary artery bypass graft (CABG), percutaneous transluminal coronary angiopatery (FTCA), stroke, tumour growth, invasion or metastasis, inflammation, septic shock, hypotension, adult respiratory distress syndrome (ARDS), arterial fibrillation and disseminated intravascular coagulopathy (DIC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a human antibody (an interleukin (IL)-4 antagonist) (I) that binds human IL-4 receptor (IL-4R), and is capable of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human, antibody, interleukin, IL-4; antagonist, receptor, IL-4 receptor, antiarthritic; dermatological; antiulcer; antiinflammatory; cytostatic; antisickling; immunosuppressive; tuberculostatic; ophthalmological;
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Pred. No. 3.2e-07;
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15-FEB-2001; 2001US-00785934.
01-MAY-2001; 2001US-00847816.
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N-PSDB; ABA94330.
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inhibiting an IL-4-induced biological activity. (I) is also useful for inhibiting both IL-4-induced biological activity and IL-13-induced biological activity in a human, and for treating septic arthritis in a human afflicted with septic arthritis. (I) is also used for treating conditions such as septic/reactive arthritis, dermatitis herpetiformis, curicaria (sepecially formic idiopathic utricaria), ulcers, gastric inflammation, mucosal inflammation, ulcerstude colitis, Crohn's disease, inflammation, mucosal inflammation, ulcerstude system in which IL-4 plays a role (e.g. IL-4-induced inflammation of part of the gastrointestinal tract), conditions in which IL-4-induced barrier colitis in the lung or gastrointestinal tract), conditions in which IL-4-induced barrier colitis in the lung or gastrointestinal tract), scleroderma, hyperplasia, IL-4-induced pulmonary conditions, allergic reactions to scleroderma, hyperplasia, IL-4-induced pulmonary conditions, allergic reactions to scleroderma, hyperplasia, in the lung or gastrointestinal tract), scleroderma, hyperplasia, in the lung or gastrointestinal processed of strauss syndrome, Grave's disease, sickle cell disease, benign prostate conditions, allergic reactions to strauss syndrome, draves and uncommune hymphopycoliferative syndrome, autoimmune hymphopycoliferative syndrome, autoimmune blistering conditions allowants, especially when directing the immunotherapy and as vacine adjuvants, especially when directing the immunotherapy and conditions that the immunotherapy and the septement sequence represents each an anti-IL-4 receptor monoclonal antibody when the immunotherapy and antibody when the 
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ches 0; Indels
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17-OCT-2000; 2000US-0240B16F.
16-MAR-2001; 2001US-02748P.
21-MAR-2001; 2001US-027379P.
25-MAY-2001; 2001US-0293499P.
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Best Local Similarity 94.1
Matches 16; Conservative
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WPI; 2002-114799/15.
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                                                                               This invention describes novel antibodies that immunospecifically bind to B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the tumour necrosis factor (TMF) super family and induces B cell cumour necrosis factor (TMF) super family and induces B cell prollferation and differentiation. The antibodies of the invention have cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antitheumatic and antiAIDS activity and can be used in vaccines to inhibit the expression and activity of BLyS. The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in biological samples and may be used in this way to diagnose disease associated with aberrant expression biological samples and may be used in this way to diagnose disease associated with aberrant BLyS expression and activity such as cancer, immune, and autoimmune disorders and diseases, e.g. systematic lumpune erythematosus, rheumatoid arthritis, immunodeficiency (e.g. common variable immunodeficiency (CVID) and acquired immunodeficiency syndrome (ALDS)). ABP41990-ABP47228 represent the antibodies described in the method of
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                        Antibodies against B Lymphocyte Stimulating polypeptides, useful for the diagnosis and treatment of cancers and immune disorders.
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                                                          Claim 1; Page 1981-1982; 3148pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human BLyS binding scFv SEQ ID 916.
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25-MAY-2001; 2001US-0293499P.
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Matches 16; Conservative
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WPI; 2002-114799/15
                                                                                                                                                                                                                                                                                                                  Sequence 248 AA;
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16-MAR-2001;
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This invention describes novel antibodies that immunospecifically bind to B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the tumour necrosis factor (TNF) super family and induces B cell proliferation and differentiation. The antibodies of the invention have cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antirhummatic and antifuls activity and can be used in vaccines to inhibit the expression and activity of BLyS. The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in biological samples and may be used in this way to diagnose disease associated with aberrant expression of BLyS. They may also be associated with aberrant expression of always with aberrant BLyS expression and activity such as cancer, immune, and autoimmune disorders and diseases e.g. systemic lupus erythematosus, rhoumatoid arthritis, immunodeficiency (e.g. common variable immunodeficiency (CVID) and acquired immunodeficiency and ragments of the antibodies described in the method of
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Antibodies against B Lymphocyte Stimulating polypeptides, useful for the diagnosis and treatment of cancers and immune disorders.
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                                                                                                                    Claim 1; Page 1495-1496; 3148pp; English.
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(CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
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17-OCT-2000; 2000US-0240816P.
16-MAR-2001; 2001US-0276248P.
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25-MAY-2001; 2001US-0293499P.
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Best Local Similarity 94.1
Matches 16; Conservative
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Exymptocyte Stimulator (BLyS) polypeptides. BlyS is a member of the tumour necrosis factor (TNF) super family and induces B cell tumour necrosis factor (TNF) super family and induces B cell proliferation and differentiation. The antibodies of the invention have cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antirheumatic and antiAIDS activity of BLyS. The antibodies bind to BLyS in hibit the expression and activity of BLyS. The antibodies bind to BLyS in biological samples and may be used in this way to diagnose disease associated with aberrant expression of BLyS. They may also be associated with aberrant syncesion of BLyS. They may also be administered to treat diseases associated with aberrant BLyS expression and activity such as cancer, immune, and autoimmune disorders and diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, immunodeficiency (e.g. common variable immunodeficiency (CVID) and acquired immunodeficiency syndrome (AIDS)). ABP43990-ABB47228 represent the antibodies and fragments of the antibodies described in the method of
                                                                                                                                                                                                                                                                                                                            antibodies that immunospecifically bind to
Antibodies against B Lymphocyte Stimulating polypeptides, useful for the diagnosis and treatment of cancers and immune disorders.
                                                                                                                                                                                            Claim 1; Page 1492-1493; 3148pp; English.
                                                                                                                                                                                                                                                                                                                     This invention describes novel
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Score 87; DB 5; Length 248; Pred. No. 9.3e-06; Mismatches 0; Indels 17 98.98; 1 IISYDGSKKYYADSVKG Conservative Query Match Best Local Similarity Local 16; Conserva Sequence 248 AA; 셤 ઠ

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Gaps

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ADG95730 standard; protein; 248 AA (first entry) 11-MAR-2004 ADG95730; RESULT

antibody; B lymphocyte stimulator; BLyS; tumour necrosis factor; B cell proliferation; differentiation; scFv; myasthenia gravis; multiple sclerosis; asthma: rheumatoid arthritis; AIDS; leukaemia; carcinoma; lymphoma; antirheumatic; antiarthritic; neuroprotective; antinflammatory; antiasthmatic; antiallergic; cytostatic. Single chain antibody that immunospecifically binds BLyS SeqID 914.

Unidentified

WO2003055979-A2

10-JUL-2003.

14-NOV-2002; 2002WO-US036496,

16-NOV-2001; 2001US-0331469P. 19-DEC-2001; 2001US-0340817P.

(HUMA-) HUMAN GENOME SCI INC.

Vaughan TJ, Hilbert D; Choi GH, Ruben SM, Barash SC,

WPI; 2003-505530/47.

Novel antibody that immunospecifically binds to a B lymphocyte stimulator (BLys), useful for detecting and treating diseases or disorders e.g. rheumatoid arthritis, asthma and leukemia.

Novel antibody that immunospecifically binds to a B lymphocyte stimulator (BLys), useful for detecting and treating diseases or disorders e.g. rheumatoid arthritis, asthma and leukemia.

Example 1; SEQ ID NO 916; 394pp; English

Example 1; SEQ ID NO 914; 394pp; English.

This invention relates to novel antibodies that immunospecifically bind to B lymphocyte stimulator (BLyS). The BLyS gene has been mapped to chromosome 1344 and encodes a protein that is a member of the tumour necrosis factor superfamily and induces both in vivo and in vitro B cell proliferation and differentiation. Specifically, it refers to single confain antibody molecules (screws) derived, preferably, from the variable heavy CDR3 region that immunospecifically bind to a polypeptide, or fragment thereof, of either human, murine, rat or monkey BLyS. The correct invention refers to the use of such antibodies in various methods for the detection, diagnosis and prognosis of diseases related to the abstrant expression or inappropriate function of BLyS or its receptor. As such, these compositions are useful for identifying immume disorders including myasthenia gravis and multiple sclerosis, inflammatory disorders e.g. asthma and rheumatoid arthritis, infectious diseases such as AIDS and proliferative disorders including leukaemia, carcinoma and lymphoma. Accordingly, they can be described as exhibiting various activities such as antirheumatic, antiallergic and cytostatic. This conjugation sequence date for this patent did not form part of the printed specification, but was obtained in electronic format confunctive the printed specification, but was obtained in electronic format. ; 0 Gaps B cell proliferation; differentiation; scrv; myasthenia gravis; multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia; carcinoma; lymphoma; antirheumatic; antiarthritic; neuroprotective; antiinflammatory; antiasthmatic; antiallergic; cycostatic Single chain antibody that immunospecifically binds BLyS SeqID 916. antibody; B lymphocyte stimulator; BLyS; tumour necrosis factor; ö Length 248; 98.9%; Score 87; DB 7; Length 248 94.1%; Pred. No. 9.3e-06; iive 1; Mismatches 0; Indels Choi GH, Vaughan TJ, Hilbert D; ADG95732 standard; protein; 248 AA. 17 99 16-NOV-2001; 2001US-0331469P. 14-NOV-2002; 2002WO-US036496. (HUMA-) HUMAN GENOME SCI INC. 50 VISYDGSKKYYADSVKG 1 IISYDGSKKYYADSVKG 11-MAR-2004 (first entry) Conservative Ruben SM, Barash SC, Local Similarity WPI; 2003-505530/47. Sequence 248 AA; WO2003055979-A2. Unidentified 10-JUL-2003. 16; ADG95732; Query Match Matches RESULT 7 ADG95732 g ઠ

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    invention relates to novel antibodies that immunospecifically bind
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Sequence 248 AA;

ö 98.9%; Score 87; DB 7; Length 248; 94.1%; Pred. No. 9.3e-06; ive 1; Mismatches 0; Indels 1 IISYDGSKKYYADSVKG 17 Query Match 98.9 Best Local Similarity 94.1 Matches 16; Conservative ઠે 용

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Gaps

ADG96139 standard; protein; 248 AA. (first entry) 11-MAR-2004 ADG96139; RESULT 8 ADG96139

Single chain antibody that immunospecifically binds BLyS SeqID 1323.

antibody; B lymphocyte stimulator; BLyS; tumour necrosis factor; B cell proliferation; differentiation; scFv; myasthenia gravis; multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia; carcinoma; lymphoma; antirheumatic; antiathritic; neuroprotective; antiinflammatory; antiasthmatic; antiallergic; cytostatic.

Unidentified

WO2003055979-A2

10-JUL-2003.

14-NOV-2002; 2002WO-US036496.

16-NOV-2001; 2001US-0331469P.

(HUMA-) HUMAN GENOME SCI INC.

Vaughan TJ, Hilbert D; Choi GH, Ruben SM, Barash SC,

WPI; 2003-505530/47.

Novel antibody that immunospecifically binds to a B lymphocyte stimulator (BLys), useful for detecting and treating diseases or disorders e.g. rheumatoid arthritis, asthma and leukemia.

Example 1; SEQ ID NO 1323; 394pp; English

Antibodies against B Lymphocyte Stimulating polypeptides, useful for the

Hilbert

Vaughan T,

Choi GH,

Ruben SM, Barash SC, WPI; 2002-114799/15.

CAMBRIDGE ANTIBODY TECHNOLOGY.

HUMAN GENOME SCI INC

(HUMA-) (CAMB-)

2001US-0277379P 2001US-0293499P

21-MAR-2001; 25-MAY-2001;

This invention relates to novel antibodies that immunospecifically bind to B lymphocyte stimulator (BLyS). The BLyS gene has been mapped to circomosome 1344 and encodes a protein that is a member of the tumour necrosis factor superfamily and induces both in vivo and in vitro B cell proliferation and differentiation. Specifically, it refers to single chain antibody molecules (scrys) derived, preferably, from the variable the average that immunospecifically bind to a polypeptide, or fragment thereof, of either human, murine, rat or monkey BLyS. The present invention refers to the use of such antibodies in various methods for the detection, diagnosis and prognosis of diseases related to the aberrant expression or inappropriate function of BLyS or its receptor. As such, these compositions are useful for identifying immune disorders including mysethenia gravis and multiple sclerosis, inflammatory disorders e.g. asthma and rheumatoid arthritis, infectious diseases such as AIDS and proliferative disorders including leukaemia, carcinoma and collymphoma. Accordingly, they can be described as exhibiting various extinitiammatory, antiasthmatic, antiallergic and cytostatic. This antiinflammatory, antiasthmatic, antiallergic and cytostatic. This invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format of the printed year of the collection of the printed specification, but was obtained in electronic format of the printed year. ö BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulan; immunomodulatory; antirheumatic; antiAIDS; vaccine; cancer; immune; tutoimmune disorder; immunodeficiency; systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS; common variable immunodeficiency; acquired immunodeficiency syndrome. Gaps ö 98.9%; Score 87; DB 7; Length 248; 94.1%; Pred. No. 9.3e-06; ive 1; Mismatches 0; Indels Human BLyS binding scFv SEQ ID 1114. ABP45103 standard; protein; 251 AA. 1 IISYDGSKKYYADSVKG 17 99 15-JUN-2001; 2001WO-US019110. 2000US-0212210P 2000US-0240816P 2001US-0276248P 19-AUG-2002 (first entry) 98.5' Best Local Similarity 94.1' Matches 16; Conservative Sequence 248 AA; WO200202641-A1. 16-JUN-2000; 17-OCT-2000; 16-MAR-2001; Homo sapiens 10-JAN-2002 ABP45103; RESULT 9 ABP45103 ò 셤

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27-SEP-2002; 2002US-0414053P
25-NOV-2002; 2002US-0428807P.
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                                                                               This invention describes novel antibodies that immunospecifically bind to B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the tumour necrosis factor (TMF) super family and induces B cell cumour necrosis factor (TMF) super family and induces B cell proliferation and differentiation. The antibodies of the invention have cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antitheumatic and antiAIDS activity and can be used in vaccines to inhibit the expression and activity of BLyS. The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in biological samples and may be used in this way to diagnose disease associated with aberrant expression of BLyS. They may also be administered to treat diseases associated with aberrant BLyS expression and activity such as cancer, immune, and autoimmune disorders and diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, immunodeficiency (e.g. common variable immunodeficiency (CVID) and acquired immunodeficiency syndrome (AIDS)). ABP43290-ABP4728 represent the antibodies and fragments of the antibodies described in the method of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antibody; B lymphocyte stimulator; BLyS; tumour necrosis factor; B cell proliferation; differentiation; scFv; myasthenia gravis; multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia; carcinoma; lymphoma; antirheumatic; antiarthritis; neuroprotective; antifilammatory; antiathmatic; antiallergic; cytostatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Single chain antibody that immunospecifically binds BLyS SeqID 1114
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diagnosis and treatment of cancers and immune disorders.
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Local Similarity 94.1%; Pred. No. 9.4e-06;
les 16; Conservative 1; Mismatches 0;
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                                           Claim 1; Page 1731-1732; 3148pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   invention
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C chromosome 1914 and encodes a procein that is a member of the tumour control of 1914 and encodes a procein that is a member of the tumour control of 1914 and encodes a procein that is a member of the tumour control of 1914 and encodes a procein that is a member of the tumour control of 1914 and encodes a procein that is a member of single control encodes a procein that is a member of 1914 and induced both in vivo and in vitro B cell control of 1914 and induced both in vivo and in vitro B cell control of 1914 and induced both in vivo and in vitro B cell control of 1914 in antibody collades (seven derived, of either human, matther action many dispersive intended by the variable control in the region that immunopecitatily bind to a polypopide, or enter that and intended by the inflamment of the compositions are useful for identifying immune disporders including myactheria gravia and multiple cell cols inflamment of a problem of including pacterial gravia and multiple cell cols inflamment of a problem of including pacterial gravia and multiple cell cols inflamment of a problem in variable compositions and remarked are administrated and cyclosarior. This colling including pacterial and including pacterial including pacterial and includin
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The present invention describes a human heterodimeric antibody (I) (fragment) having a binding affinity of at least 1x10-8 M to the protective antigen of Bacillus anthracis or a molecule involved in anthrax infection that blocks binding of the antigen or molecule to receptors, edema factor and lethal factor. (I) has virucide and antibacterial activities, and can be used in immunotherapy. The antibodies (I) are useful as anti-toxins or anti-infectives with respect to infective agents, such as anthrax, botulinum, smallpox, Venezuelan equine encephalomyelltis virus (VESV), or West Nile virus (WNV). The present sequence represents a human heterodimeric antibody heavy chain variable region amino acid sequence, which is used in the exemplification
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention provides a neuromodulatory agent (I) capable of promoting neurite outgrowth, regeneration, remyelination and neuroprotection in central nervous system (CNS). (I) is capable of inducing remyelination, promoting cellular proliferation of glial cells, and promoting Ca2+ signaling with oligodendrocytes. An humanised antibody to (I) can be selected from antibody sHIGMS (LWM 22), beVHIGM MSI19D10, ebv HIGM CB2bGB, AKJR4, CB2iBI2, CB3LB7 or MSI19BS. (I) is useful for stimulating remyelination of CNS axons, stimulating proliferation of glial cells in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel neuromodulatory agent (a human IgM monoclonal antibody), promoting neurite outgrowth, regeneration, remyelination and neuroprotection in central nervous system, useful to treat post-infectious
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Neuromodulatory, central nervous system; CNS; sH1gM22; LYM 22; AKJR4; ebvHigM MsI19D10; ebv H1gM CB2bG8; CB2iE12; CB2iE7; MSI19E5; virucide; antiparkinsonian; neuroprotective; nootropic; vulnerary.
                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                               Length 135;
                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sHigM22 heavy chain variable region clone B sequence.
                                                                                                                                                                                                                                                                                                                               97.7%; Score 86; DB 7; 94.1%; Pred. No. 6.8e-06;
                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MAYO-) MAYO FOUND MEDICAL EDUCATION RES.
                   Claim 11; SEQ ID NO 97; 67pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pease LR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABB07186 standard; protein; 119 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 23; Fig 17; 219pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                             30-MAY-2000; 2000WO-US014902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10-MAY-2000; 2000US-00568351
                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 94...
Local 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                        1 IISYDGSKKYYADSVKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                           of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rodriguez M, Miller DJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2002-066596/09.
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                                                                                                                                                                                                                                                                                             Sequence 135 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABB07186;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABB0718
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                                                                   TWEEV) Or for treating a human being having multiple sclerosis, or a human or domestic animal with a viral demyelinating disease, or a postneural disease of CNS. (T) is also useful for an in vitro method of tetimulating the proliferation of glial cells from mixed cell culture. (I) is also useful for mixed cell culture. (I) is also useful for mixed cell culture. (I) set mulating the proliferation of colls axons. The antibodies are useful for preventing infection by a bacterium, virus or like pathogen that causes demyelination or other neurodegenerative condition in a subject. Methods where (I) is administered to a patient are useful for treating multiple sclerosis, Parkinson's disease, Alzheimer's disease, amyotrophic lateral sclerosis (ALS), a viral demyelinating disease, CNS diseases, and other conditions in the CNS where nerves are chain variable region clone B amino acid sequence
CNS axons, or treating demyelinating disease of CNS in a mammal in need cf such therapy. (I) is capable of binding to structures and cells within CNS. (I) is preferably useful for treating a demyelinating disease of CNS of a mouse infected with Strain DA of Theiler's murine encephalomyelities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention describes an immunopolypeptide comprising a polypeptide that binds to human glucose-6-phosphate isomerase (GPI). The methods and compositions are used for diagnosis and treatment of human autoimmune disease, e.g., human rheumatoid arthritis. This is the amino acid sequence of human anti-GPI-antibody heavy chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Immunopolypeptide for diagnosis and treatment of human autoimmune disease, e.g., human rheumatoid arthritis, comprises a polypeptide that binds to human glucose-6-phosphate isomerase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human, anti-glucose-6-phosphate isomerase-antibody, immunopolypeptide, anti-GPI-antibody, GPI; glucose-6-phosphate isomerase; autoimmune disease, rheumatoid arthritis; heavy chain variable region, VH; complementarity determining region; CDR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Anti-GPI-antibody heavy chain complementarity determining region #10.
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                                                                                                                                                                                                                                                                                                                                                                                                       96.6%; Score 85; DB 5; Length 119; 94.1%; Pred. No. 8.6e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 3; Fig 4A; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 IISYDGSKKYYADSVKG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-SEP-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                               16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-521517/49.
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Matches 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (BURT/) BURTON D R. (SCHA/) SCHALLER M.
                                                                                                                                                                                                                                                                                                                                                                 Sequence 119 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US2002146753-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AB033850;
                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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Matches

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The invention provides a neuromodulatory agent (I) capable of promoting central nervous system (CNS). (I) is capable of inducing remyelination, central nervous system (CNS). (I) is capable of inducing remyelination, promoting cellular proliferation of glial cells, and promoting Ca2+ capable of promoting central nervous system (CNS). (I) is capable of inducing remyelination, cellular proliferation of glial cells, and promoting Ca2+ capable of binding proliferation of (I) can be selected from antibody sHIGMS2 (LVM 22), ebvHigh Marl9D10, ebv High CSD268, AKJR4, CB21E12, CB21E7 or MSI19E5. (I) is useful for stimulating cempelination of CNS axons, or treating demyelinating disease of CNS in a mammal in need of such therapy. (I) is capable of binding to structures and cells within CNS. (I) is preferably useful for treating a demyelinating disease of CNS. (CNS) is a mountain in the proliferation of Theiler's murine encephalomyelitis (TMEV) or for treating a human being having multiple sclerosis, or a post-numan or domestic animal with a viral demyelinating disease, or a post-numal disease of CNS. (I) is also useful for an in vitro method of care useful for stimulating remyelination of CNS axons. The antibodies are useful for stimulating remyelination of CNS axons. The antibodies corrected the proliferation of other neurodegenerative condition of the reacting multiple sclerosis, Parkinson's disease, Alzheimer's disease, amyotrophic lateral sclerosis (ALS), a viral demyelinating changed as by trauma. The present sequence represents the shights heavy conditions in the CNS where nerves are chain variable region clone A amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel neuromodulatory agent (a human IgM monoclonal antibody), promoting neurite outgrowth, regeneration, remyelination and neuroprotection in central nervous system, useful to treat post-infectious
                                                                                                                            Neuromodulatory; central nervous system; CNS; sHIGM22; LYM 22; AKJR4; ebvHigM MsI19D10; ebv HIGM CB2bG8; CB2iE12; CB2iE7; MSI19E5; virucide; antiparkinsonian; neuroprotective; nootropic; vulnerary.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 84; DB 5; Length 119
Pred. No. 1.3e-05;
2; Mismatches 0; Indels
                                                                                     BHigM22 heavy chain variable region clone A sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                             (MAYO-) MAYO FOUND MEDICAL EDUCATION RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rodriguez M, Miller DJ, Pease LR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 23; Fig 17; 219pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                               10-MAY-2000; 2000US-00568351.
                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      encephalomyelitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; ABA94216
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                                                                                                                                                                                                                                                                  WO200185797-A1.
                                                                                                                                                                                                                         Homo sapiens
                                           13-MAR-2002
                                                                                                                                                                                                                                                                                                              15-NOV-2001
  ABB07169;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Immunopolypeptide for diagnosis and treatment of human autoimmune disease, e.g., human rheumatoid arthritis, comprises a polypeptide that binds to human glucose-6-phosphate isomerase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; anti-glucose-6-phosphate isomerase-antibody; immunopolypeptide; anti-GPI-antibody; GPI; glucose-6-phosphate isomerase; autoimmune disease; rheumatoid arthritis; heavy chain variable region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                Score 84; DB 7; Length 17;
Pred. No. 1.4e-06;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human anti-GPI-antibody heavy chain variable region #3.
                                                                                                                              2; Mismatches
                                                                                                                                                                                                                                                                                                                                   ABO33836 standard; protein; 112 AA
complementarity determining region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schaller M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 11; Fig 3AH; 47pp; English.
                                                                                                                                                                                                    1 IISYDGSKKYYADSVKG 17
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                                                                                   95.5%;
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                                                                                                                                 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (BURT/) BURTON D R. (SCHA/) SCHALLER M.
                                                                                   Query Match
Best Local Similarity
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Best Local Similarity
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                                           Sequence 17 AA;
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Gaps

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October 14, 2005, 16:12:39

Job time : 132.688 secs

Search completed:

ABB07169 standard; protein; 119 AA.

ABB07169 ID ABB0 XX

Matches

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Length 119;

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Compugen Ltd.
GenCore version (c) 1993 - 2005
           Copyright
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- protein search, using sw model OM protein

October 14, 2005, 16:02:59; Search time 23.6406 Seconds (without alignments) 69.190 Million cell updates/sec Run on:

US-10-614-959-11 88 Title: Perfect score:

1 IISYDGSKKYYADSVKG 17

Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283416 segs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

283416

seq length: 0 seq length: 200000000 88 Minimum Maximum

summaries Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 su

PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		de			SUMMARIES		
Result No.	Score	Query	Length	DB	ID	Description	
-	82	93.2	94	7	PL0120	heavy	-
7	82	93.2	97	7	S44115		>
9	82	93.2	98	~	PL0116	heavy	<u>-</u>
4	82	93.2	98	~	S29546	_	>
S	82	93.2	109	~	PH1646	heavy	>
9	82	93.2	109	N	PH1644	heavy	>
7	82	93.2	111	~	PH1643	heavy	>
æ	82	93.2	111	~	PH1645	heavy	>
6	82		113	ď	S38490	heavy	,
10	82	93.2	114	~	S46390		>
11	82	93.2	114	~	846392	heavy	>
12	82	m	117	~	S36270	heavy	>
13	82		118	~	S31677	heavy	>
14	82	93.2	118	7	831116	heavy	'
15	82	93.2	119	~	F36005	heavy	>
16	82		120	7	831112	heavy	,
17	82	93.2	121	~	S19666	heavy	>
18	82	•	121	~	G36005	heavy	>
19	82	93.2	122	~	E36005	heavy	>
20	82	93.2	122	~	S31119	heavy	<u>'</u>
21	82	93.2	123	~	S38493	heavy	•
22	82		130	~	PL0098	heavy	Pr
23	82	93.2	132	~	S31603	heavy	>
24	82	93.2	134	~	831679	heavy	>
25	82	ë.	139	~	S31674	heavy	>
26	77	87.5	137	~	831701	heavy	>
27	75	٠	108	~	9	heavy	>
28	75	85.2	114	~	63	heavy	>
29	75	85.2	119	~	S31111		•

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19 heavy chain V region - human

19 heavy chain V region - human

2) Species: How sapiens (man)

2) Accession: S44115

3) Hawkins, R.E.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.

3) Submitted to the EMBL Data Library, March 1994

A. Pescription: Idiotypic vaccination against human B-cell lymphoma: rescue of variable r

A, Reference number: S44105

A, Reference number: S44115

A, Accession: S44115

A, Residues: DNA

A, Residues: 1-97 < HAWA

A, Residues: 1-97 < HAWA

A, Residues: 1-97 < HAWA

A, Cross-references: EMBL: Z31384; NID: 9472969; PIDN: CAA83259.1; PID: 9940526

C, Superfamily: Immunoglobulin V region; Immunoglobulin homology

C, Keywords: heterotetramer; immunoglobulin

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Gaps

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Query Match
93.2%; Score 82; DB 2; Length 97;
Best Local Similarity 88.2%; Pred. No. 7.5e-06;
Matches 15; Conservative 1; Mismatches 1; Indels

		~	heavy chain	heavy	heavy chain	heavy chain	heavy chain	_	Ig heavy chain V r						
831117	S48797	A49028	831510	S29543	836259	PH1662	M3HUAM	S31688	831598	S70442	A60943	S36284	PH1661	PH1660	831592
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22	128	133	133	86	117	118	122	134	135	140	151	115	121	118	9/
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85.2 1	85.2	85.2	85.2	84.1	84.1	84.1	84.1	84.1	84.1	84.1	83.0	81.8	81.8	80.7	78.4
85.2	_	75 85.2	_	_	_	_	_	_	_	_	_	81	_	8	7

ALIGNMENTS

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C;Accession: PL0120
R;Bird, J.; Gallli, N.; Link, M.; Stites, D.; Sklar, J.
J. Exp. Med. 168, 229-245, 1988
A;Title: Continuing rearrangement but absence of somatic hypermutation in immunoglobulin A;Reference number: PL0116; WUID:88286083; PMID:2840480
                                                                                                                                                                                                                                                                                                                                                                                                            A; Cross-references: UNIPROT: QBWUK1; UNIPROT: Q9UL93
A; Experimental source: B cells from patient TD with acute lymphoblastic leukemia, ALL
A; Experimental source: B cells from patient TD with acute lymphoblastic leukemia, ALL
A; Note: the sequence shows the V region (TD-Vo) from a nonproductive DNA rearrangement f
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: acute lymphoblastic leukemia; heterotetramer; immunoglobulin
F; 31-35/Region: complementarity-determining 1
F; 49-65/Region: complementarity-determining 2
                                                                     C;Species: Homo sapiens (man)
C;Date:`07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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88.2%; Pred. No. 7.2e-06;
tive 1; Mismatches 1; Indels
PL0120
Ig heavy chain V-III region (TD-Vo) - human (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 IISYDGSKKYYADSVKG 17
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les 15; Conserv
                                                                                                                                                                                                                                                                                                              A;Accession: PL0120
A;Molecule type: mRNA
A;Residues: 1-94 <BIR>
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Matches
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SO VISYDGSNKYYADSVKG 66

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RESULT 2

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Ig heavy chain V region (clone 6H12) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 09-Jul-2004
C;Accession: PH1646
R;Hillson, JL.; Karr, N.S.; Oppliger, I.R.; Mannik, M.; Sasso, E.H.
J. Exp. Med. 178, 331-336, 1993
A;Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphylo A;Reference number: PH1642; MUID:93301610; PMID:8315388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Accession: PH1644

C;Accession: PH1644

J. Exp. Ned. 176, 331-336, 1993

J. Exp. Ned. 176, 331-336, 1993

A;Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphylo A;Reference number: PH1642; MUID:93301610; PMID:8315388

A;Accession: PH1644

A;Residues: 1-109 < HIL>
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R;Hillson, J.L.; Karr, N.S.; Oppliger, I.R.; Mannik, M.; Sasso, E.H.
A;Tile: The structural basis of germline-encoded VH3 immunoglobulin binding to staphylo A;Reference number: PH1642; MUID:93301610; PMID:8315388
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IG heavy chain V region (clone 6H7) - human (fragment)
C.Species: Homo sapiens (man)
C.Species: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Homo sapiens (man)
C;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 09-Jul-2004
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C, Superfanily: immunoglobulin V region; immunoglobulin homology
C, Keywords: heterocteramer; immunoglobulin
F;7-90/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: UNIPROT:Q8WUK1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;7-90/Domain: immunoglobulin homology <IMM>
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                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 82; DB 2; I Pred. No. 8.4e-06;
Pred. No. 7.5e-06;
1; Mismatches 1
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                                1,
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Best Local Similarity 88.2%;
Matches 15; Conservative
   88.28;
                                                                                                                                              SO VISYDGSNKYYADSVKG
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                                                                                                   1 IISYDGSKKYYADSVKG
Best Local Similarity 88.2
Matches 15, Conservative
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Best Local Similarity
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A; Residues: 1-109 <HIL>
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PLOLICE
PLOLICE
C'Species: Homo sapiens (man)
C'Accession: PLO116; S26892
R'Bird, J. Gallill, N.; Link, M.; Stites, D.; Sklar, J.
Skpiard, J.; Gallill, N.; Link, M.; Stites, D.; Sklar, J.
Skpiard, J.; Gallill, N.; Link, M.; Stites, D.; Sklar, J.
Skpeciescen number: PLO116; MUID:88286083; PMID:2840480
A; Reference number: PLO116; MUID:88286083; PMID:2840480
A; Residues: 1-98 REIR>
A; Residues: 1-98 REIR-SI2349; MID:93021117; PMID:1404388
A; Residues: 1-98 CTOM>
A; Residues: 1-98 CTOMPODIARIC Petermining 2
B; 31-35 Region: complementarity-determining 2
F; 31-35 Region: complementarity-determining 2
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Or-Jan-1994 #sequence_revision 17-Nov-1995 #text_change 23-Jul-1999
C;Accession: S29546; S26888
R;Tomlinson, M.; Walter, G.; Cook, G.P.; Winter, G.
submitted to the EMBL Data Library, October 1992
A;Reference number: S29543
A;Accession: S29546
A;Molecule type: DNA
A;Residues: 1-98 «TOM>
A;Residues: 1-98 «TOM>
A;Residues: L-98 «TOM>
A;Residues: L-98 «TOM>
A;Residues: Data Library, NID:932843; PIDN:CAA78997.1; PID:932844
A;Residues: L-98 «TOM>
A;Accession: S26888
A;Accession: S26888
A;Accession: S26888
A;Status: preliminary
A;Accession: S26888
A;Status: preliminary
A;Accession: S26888
A;Status: preliminary
A;Accession: S26888
A;Cross-references: EMBL:Z12346; NID:932912; PIDN:CAA78216.1; PID:932913
A;Residues: 1-98 «TO2>
A;Cross-references: EMBL:Z12346; NID:932912; PIDN:CAA78216.1; PID:932913
A;Residues: L-98 «TO2>
A;Reywords: heetrotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology < IMM>
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Pred. No. 7.5e-06;
1; Mismatches 1; Indels
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                                   93.2%;
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Best Local Similarity 88.23
Matches 15; Conservative
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Query Match 93.2%; Score 82; DB 2; I Best Local Similarity 88.2%; Pred. No. 8.6e-06; Matches 15; Conservative 1; Mismatches 1;

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1 IISYDGSKKYYADSVKG 17

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C,Accession: S36270
R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J. R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J. A;Griffiths, A.D.; Ms. A;Hitle: Human anti-self antibodies with high specificity from phage display libraries. A;Reference number: S36256; MUID:93178448; PMID:7679990
                 C;Species: Homo sapiens (man)
C;Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 20-Jun-2000
C;Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 20-Jun-2000
C;Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 20-Jun-2000
B;Pigini, M.; Marks, J.D.; Winter, G.; Griffiths, A.D.
J; Mol. Biol. 239, 68-78, 1994
A;Pitle: In vitro assembly of repertoires of antibody chains on the surface of phage by A;Accession: 846390
A;Accession: 846390
A;Acture: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rifigini, M.; Marks, J.D.; Winter, G.; Griffiths, A.D.
J. Mol. Blol. 239, 68-78, 1994
A;Title: In vitro assembly of repertoires of antibody chains on the surface of phage by A;Reference number: $46390; MUD:94254092; PMID:8196048
A;Accession: 546392
A;Status: preliminary
A;Molecule type: DNA
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C,Superfamily: immunoglobulin V region; immunoglobulin homology
C,Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Homo sapiens (man)
C;Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 20-Jun-2000
C;Accession: S46392
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C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL: Z31686; NID: 9509782; PIDN: CAA83491.1; PID: 91335143
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C;Keywords: heterotetramer; immunoglobulin
F;IS-98/Domain: immunoglobulin homology <IMM>
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Pred. No. 8.8e-06;
1; Mismatches 1; Indels
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A;Residues: 1-117 <GRI>
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Pred. No. 8.8e-06;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ig heavy chain V region (VH-28) - human
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50 VISYDGSNKYYADSVKG 66
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Best Local Similarity 88.2%;
Matches 15; Conservative
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Local Similarity 88.2%;
nes 15, Conservative
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Ig heavy chain V region - human
                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-114 <FIG>
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$33490
Ig heavy chain - human (fragment)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C; Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C; Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C; Date: 06-Jan-1995 #sequence_revision: S38490
R; Marks, J.D; Ouwehand, W.H.; Bye, J.M.; Finnern, R.; Gorick, B.D.; Voak, D.; Thorpe, Submitted to the EMBL Data Library, June 1993
A; Reference number: S38488
A; Reference number: S38488
A; Reference number: S38490
A; Residues: 1-113 <ARR>
A; Nolecule type: DNA
A; Residues: 1-113 <ARR>
A; Residues: 1-113 <ARR>
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Reywords: heterotetramer; immunoglobulin
F; 15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PH1645

PH1645

PH1645

Grady chain V region (clone 6C8) - human (fragment)

C;Species: Homo sapiens (man)

C;Species: Homo sapiens (man)

C;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 09-Jul-2004

C;Accession: PH1645

R;Hillson, J.L; Karr, N.S.; Oppliger, I.R.; Mannik, M.; Sasso, E.H.

J. Exp. Med. 178, 331-336, 1993

A;Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphylc

A;Reference number: PH1642; MUID:93301610; PMID:8315388
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A;Residues: 1-111 <HIL>
A;Residues: 1-111 <HIL>
A;Cross-references: UNIPROT:QSWUK1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heteroterramer; immunoglobulin
F;7-90/Domain: immunoglobulin homology <IMM>
                               A;Residues: 1-111 <HIL>
A;Cross-references: UNIPROT:Q8WUK1
C;Superfamily: immunoglobulin v region; immunoglobulin homology
C;Keywords: heteroterramer; immunoglobulin
F;7-90/Domain: immunoglobulin homology <IMM>
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1 IISYDGSKKYYADSVKG 17

A; Accession: PH1645

RESULT 10 S46390

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15; Conservative

Query Match Best Local 8

Matches

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Length 119 1; Indels

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A;Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene
A;Reference number: A36005; MUID:90349571; PMID:2117273
A;Accession: F36005
                                                                                                                                                                                                                                                                                                 A;Cross-references: GDB:118731; OMIM:146910
A;Map position: 14q22.33-14q32.33
C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heteroteramer; immunoglobulin P:15-98/Domain: immunoglobulin homology <IMM>
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88.2%; Pred. No. 9.2e-06;
tive 1; Mismatches 1;
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C;Genetics:
A;Gene: GDB:IGH@; IGHDY1
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Best Local Similarity 88.23
Matches 15; Conservative
                                                                                                               A,Status: preliminary
A,Molecule type: mRNA
A,Residues: 1-119 <SCH>
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C;Species: Homo sapiens (man)
C;Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 09-Jul-2004
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                   Score 82; DB 2; Length 117;
Pred. No. 9e-06;
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Pred. No. 9.1e-06;
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C;Date: 21-Dec-1990 #sequence_revision 21-Dec-1990
C;Accession: F36009
R;Schreder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
                                                                              1; Mismatches
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Best Local Similarity 88.2%;
Matches 15; Conservative
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                                              October 14, 2005, 15:51:44; Search time 113.156 Seconds (without alignments) 76.932 Million cell updates/sec
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Q8wuk1
Q9u190
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Q6n093
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Q9y509
Q9x509
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Q9n106
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Q6pja4
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Q9ul72
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Q6n097
Q6mzu6
Q96bb9
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      GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                              1612378 seqs, 512079187 residues
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                                                                                                                                                                                                                                                                                                       090L93
0665C9
0865C9
0865C9
080L90
040093
068CN4
068CN4
07251
072351
080CL6
072351
080CL6
090L84
HV3L HUWAN
090LB6
090LB6
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Q9UL72
HV05 CARAU
HV3K_HUMAN
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Q6DDQ7
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HV3F HUMAN
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Maximum Match 100%
Listing first 45 summaries
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                                  OM protein - protein search, using sw model
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Q6MZU6
Q96BB9
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Q6N0<u>9</u>2
Q9UL71
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Gapop 10.0 , Gapext 0.5
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                                                                                          1 IISYDGSKKYYADSVKG 17
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1: uniprot_sprot:*
2: uniprot_trembl:*
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Maximum DB seq length: 2000000000
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88
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Match Length DB
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Perfect score:
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25-0CT-2004 (TrEMBLrel. 28, Last sequence update)
25-0CT-2004 (TrEMBLrel. 28, Last annotation update)
Single-chain Fv (Fragment).
Name=scFv;
Name=scFv;
Homo saplena (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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06in78
06mzq6
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065px4
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099y171
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P01764
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MEDINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531; MAD.K., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
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Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL; AF035021; AAD56257.1; -..
PIR; PH1644; PH1644.
PIR; PL0120; PL0120.
HSSP; P01772; ZFB4.
InterPro; IPR007110; Ig-like.
InterPro; IPR007110; IRR; I.
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88.2%; Pred. No. 1e-05;
iive 1; Mismatches
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Q61N78
Q6MZQ6
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Q6GMZ2
Q65ZL8
Q920E7
Q9GJ71
Q9GJ71
Q9AV03
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(Fragment).
Mono sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE PROM N.A.
MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531; M.X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
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113 AA; 12437 MW; ED57FDD19086D07F CRC64;
                                                                                                                                                                                                                                                                                                                                                         SMART; SMO0406; IGV; 1.
PROSITE; PSSOB35; IG LIKE; S.
PROSITE; PSO0290; IG MCI, UNKNOWN 3.
SEQUENCE 613 AA; 67295 MW; 60C7F5950671E315 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  fetus.",
Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL; AP035024; AAD56260.1; -.
PIR; S78486; S78486.
HASSP; POIT72; 2FB4.
InterPro; IPR00710; Ig-like.
InterPro; IPR003596; Ig-v.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93.2%; Score 82; DB 2; L
88.2%; Pred. No. 6.4e-05;
iive 1; Mismatches 1;
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PIR, PH1642, PH1642.
PIR, PH1643, PH1643.
PIR, PH1645, PH1645.
PIR, PH1646, PH1646.
PIR, PL0098, PL0098.
PIR, S10120, PL0120.
PIR, S31116, S31116.
PIR, S31119, S31119.
PIR, S70442, S70442.
HSSP, P01861, 1ADQ.
PERM, PF07654, C1-8et, 4.
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MEDINE-2138257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MINDLINE-21388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MINDLINE-21388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MINDLINE-21388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MINDLINE-21388257; PubMed=18.4., Grounder C.F., Bhat N.K.,

MINDLINE R.F., Jordan H., Moore T., Max S.I., Wang J., Haidh F.,

MINDLINE R.F., Jordan H., Moore T., Max S.I., Wang J., Haidh F.,

MINDLINE R.F., Jordan H., Moore T., Max S.I., Wang J., Haidh F.,

MINDLINE R.F., Jordan H., Moore T., Max S.I., Wang J., Haidh F.,

MINDLINE R.F., Jordan H., Moore T., Marken R.D., Millahy S.J.,

MINDLINE R.F., Morey D.M., Poerers G.J., Abramson R.D., Millahy S.J.,

MINDLINE R.F., Muray D.M., Sodergen B.J., Lu X., Gibbs R.A.,

MINITING M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

MINITING M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

MINITING M., Madan A., Young A.C., Schmutz J., Myers R.M., Butterfield Y.S.,

MINITING M., M., TOUChman J. W., Green B.D., Dickson M.C.,

MINITING M. M., Madan A., Xoung A.C., Schmutz J., Myers R.M., Butterfield Y.S.,

MINITIAN M. M., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

MINITIAL M. M., Madan M., M., Madan M., Rodriguez S.J., Marra M.A.,

M. Generation and initial analysis of more than 15,000 full-length human
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 93.2%; Score 82; DB 2; Length 240; Best Local Similarity 88.2%; Pred. No. 2.3e-05; Matches 15; Conservative 1; Mismatches 1; Indels
                                                                               | STRAIN=CIG/7; | MEDLINE=9736279; | MEDLINE=97362799; | PubMed=9219263; | MEDLINE=97362799; | PubMed=9219263; | MEDLINE=97362799; | PubMed=9219263; | MEDLINE=97362799; | Midter G.; | Mid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strausberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC020240; AAH20240.1; -.
PIR; F36005; F36005.
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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TISSUE=Primary B-Cells;
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Homo sapiens (Human).
                                                                SEQUENCE FROM N.A.
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      NCBI_TaxID=9606;
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Q8WUK1
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PROSITE; PS50835; IG LIKE; 3.
PROSITE; PS00290; IG MHC; UNKNOWN_2.
Hypothetical protein.
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22 VIAYDGSTQYYADSVRG 38
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                                                                                                                                                                                                Query Match
Best Local Similarity 70.6%;
Marches 12; Conservative
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1es 12; Conservative
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A Lehman D.W., Putnam F.W.;
Lehman D.W., Putnam F.W.;
Lehman D.W., Putnam F.W.;
Location of a sequence of the variable region of a human mu chain:
Tocation of a possible JH segment.";
Proc. Natl. Acad. Sci. U.S.A. 77:3239-3243(1980).

L PROC. Natl. Acad. Sci. U.S.A. 77:3239-3243(1980).

- I- MISCELLANEOUS: This mu chain was isolated from the plasma of a patient with macroglobulinemia.

- SIMILARITY: Contains 1 immunoglobulin-like domain.

R PIR; A02051; M3HUAM.

R RSP; P01772; 2FR4.

GO; GO:00058576; C:extracellular; NAS.

GO; GO:0006955; P:immune response; NAS.

R GO; GO:0006955; P:immune response; NAS.

R InterPro; IPR00110; Ig-like.

R InterPro; IPR00150; Ig-v.

R FMART; SM00406; IGv: 1.
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                                                                           Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalita; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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THO German Human CDNA Consortium;

Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,

Fobo G., Han M., Wiemann S.;

Submitted (ANG-2003) to the EMBL/GenBank/DDBJ databases.

EMBL; BX640623; CAE45777.1; -.

HSSP; P01861; 1ADO.
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Pyrrolidone carboxylic acid.
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122 AA; 13668 MW; A42D0F17D252F1C2 CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein DKFZp686I04196 (Fragment).
Name=DKFZp686I04196;
Homo sapiens (Human).
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Direct protein sequencing; Immunoglobulin V region;
Pyrrolidone carboxylic acid.
05-JUL-2004 (Rel. 44, Last annotation update) Ig heavy chain V-III region CAM. Homo sapiens (Human).
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Interpro; IPR007110; Ig-11ke.
Interpro; IPR003597; Ig_c1.
Interpro; IPR003506; Ig_Wt.
Interpro; IPR003596; Ig_v.
Pfam; PF07654; C1-8et; 3.
SWART; SW00409; IG; 2.
SWART; SW00407; IGc1; 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 IISYDGSKKYYADSVKG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE PROM N.A
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NON_TER
SEQUENCE
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                                                                                                                           Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-Rectum tumor;
The German cDNA Consortium;
The German cDNA Consortium;
Blocker H., Boecher M., Brandt P., Mewes H.W., Weil B., Amid C.,
A Osanger A., Fobo G., Han M., Wiemann S.;
Lushitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; CRY-94861; CAH18705.1;
R EMBL; CRY-94861; CH18705.1;
R InterPro; IPR001359; Ig.
R Ffam; PF00164; Ig.
R Ffam; PF00164; Ig.
R Ffam; PF00164; Ig.
R SWART; SM00409; IG.
R PROSITE; PS50835; IG_MRC; UNKNOWN_2.
R PROSITE; PS50835; IG_MRC;
W MPDChhetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaro ottori, Metarcas, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                    Length 417;
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                                    80.7%; Score 71; DB 2; Length 41.
70.6%; Pred. No. 0.0029; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         79.5%; Score 70; DB 2; Length 493
70.6%; Pred. No. 0.0052;
NON TER 1 1 SEQUENCE 417 AA, 46061 MW; C4518E844CFB883C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE 493 AA; 54117 MW; AIE4F5ED3FA8AB40 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical protein DKFZp686E23209 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                      493 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
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TISSUE=Mammary gland;
Isogai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T.,
Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K.,
Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahari K.,
Masuho Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N.,
Hattori A., Okumura K., Iwayanagi T., Ninomiya K.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
HNSSP; P01875; 10W0
                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Young D.C.; "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-CT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ch 75.0%; Score 66; DB 2; Length 122; 1 Similarity 81.2%; Pred. No. 0.0053; 13; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 493;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SWART; SW00406; IGV; 1.
PROSITE; PSS0835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; UNKNOWN 1.
SEQUENCE 493 AA; 53224 MW; 12ECD7E094777101 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        122 AA; 13579 MW; 36054D41366545B8 CRC64;
                       01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            76.1%; Score 67; DB 2; 70.6%; Pred. No. 0.016; Live 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cin. Immunol. Immunopathol. 87:184-192(1998).
EMBL, AF035630, AAD56266.1; -.
EMBL, PRO721, 2FB4.
InterPro; IPR007110; Ig-like.
InterPro; IPR0073596; Ig-v.
InterPro; IPR00406; Ig-v.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               122 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                           Hypothetical protein FLJ90170.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Interpro; IPR007110; Ig-like.
Interpro; IPR003597; Ig cl.
Interpro; IPR003056; Ig_MHC.
Interpro; IPR003596; Ig_V.
Pfam; PF07654; Cl-set; Z.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12; Conservative
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Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                        Cao J., Vescio R.A., Rettig M.B., Hong C.H., Kim A., Lee J.C.,
Lichtenstein A.K., Berenson J.R.;
"A CD10-positive subset of malignant cells is identified in multiple
myeloma using PCR with patient-specific immunoglobulin gene primers.";
Leukemia 9:1948-1953(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                 EMBL; S80860; AAD14339.1; -.
HSSP; P01847; JAQK
GQ; GQ: 0005887; C:integral to plasma membrane; NAS.
GQ; GQ: 0016066; P:cellular defense response (sensu Vertebrata); NAS.
InterPro; PR000719; Ig-like.
InterPro; IPR0007596; Ig-v.
SMART; SM00406; IGV; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Human rectum tumor;
Bloecker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BX538118; CAD98026.1; --
HSSP; P01857; 1HZH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Pred. No. 0.016;
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SEQUENCE 482 AA; 52852 MW; EDA75F1901D1A034 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 147 AA; 15768 MW; 8489FCAAA7BC925C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein DKFZp686N02209.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               493 AA.
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PROSITE; PS00290; IG_MHC; UNKNOWN_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
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                                                                                LINE=96071149; PubMed=7475288;
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InterPro; IPR003597; Ig_c1.
InterPro; IPR003306; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PP07654; C1-set; 3.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            :|||||| :|||| 50 LISYDGSTQYYAGSVKG 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS50835; IG LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 IISYDGSKKYYADSVKG 17
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70.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 78.4
Best Local Similarity 76.5
Matches 13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
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Best Local Similarity
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                                                     SEQUENCE FROM N.A
NCBI_TaxID=9606;
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SEQUENCE
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QBNCL6
ID QBNCL6
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Q7Z351
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Florent G., Lehman D., Putnam F.W.;
"The switch point in mu heavy chains of human IgM immunoglobulins.";
"Blochemistry 13:2482-2489(1974).
"In MISCELLANEOUS: This chain was isolated from a Waldenstrom's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HV3H HUMAN STANDARD; PRT; 122 AA.
P01769;
21-JUL-1986 (Rel. 01, Last sequence update)
21-JUL-1986 (Rel. 01, Last sequence update)
52-JUL-2004 (Rel. 44, Last annotation update)
19 heavy chain V-III region GA.
IG heavy chain V-III region GA.
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                          72.7%; Score 64; DB 2; Length 95; 75.0%; Pred. No. 0.0087; ive 1; Mismatches 3; Indels
                                                                                                                                                                                                                                             Length 95;
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Pyrrolidone carboxylic acid.
                    HSSP; P01820; 1G7J.
InterPro; IRR007110; 1g-like.
InterPro; IRR007110; 1g-like.
SMART; SMO0406; IGV; 1.
PROSITE; PS50815; IG_LIKE; 1.
NON_TER 1 1 1
NON_TER 95 95
SEQÜENCE 95 AA, 10527 MW, 90A8C6D16D22574A CRC64;
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122 AA; 13166 MW; 74E5B6959E84100A CRC64;
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SMART; SW00406; IGv; 1.
PROSITE; PSS0835; IG_LIKE; 1.
Direct protein sequencing; Immunoglobulin V region;
Pyrrolidone carboxylic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=74175307; PubMed=4208843;
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                                                                                                                                                                                                                                Query Match
Best Local Similarity 75.0%
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PIR; S36280; S36280.
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NON TER
SEQUENCE
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Q6PJA4;
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HV3H_HUMAN
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MEDLINE=79151016; PubMed=107164;

MEDLINE=79151016; PubMed=107164;

MITTALE STRUCTURE of a Minan 19A1 immunoglobulin. IV. Streptococcal 19A1 protease, digestion, Fab and Fc fragments, and the complete amino acid sequence of the alpha 1 heavy chain.";

J. Biol. Chem. 254.2865-2874(1979).

J. Biol. Chem. 254.2865-2874(1979).

J. SINILARITY: Contains 1 immunoglobulin-like domain.

PIR; A02056; AlHUBR.

RSSP: PO1772; PRB.

RGO; GO:000576; C:extracellular; NAS.

RO; GO:000576; C:extracellular; NAS.

RO; GO:0005576; C:extracellular; NAS.

RO; GO:0005576; C:extracellular; NAS.

RO; GO:0004913; F:immune response; NAS.

InterPro; IPR00110; Ig-like.

REPART PROMONT: Ig-like.

REPART PROMONT: Ig-like.

REPART PROMONT: Ig-like.

REPART PROMONT: Ig-like.
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Q1-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2004 (TrEMBLrel. 26, Last annotation update)
Imunoglobulin heavy chain (Fragment).
Enkaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS50835; IG LIKE; 1.
Direct protein sequencing; Glycoprotein; Immunoglobulin V region;
Pyrrolidone carboxylic acid.
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Pyrrolidone carboxylic acid.
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Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AB035268; BAA87067.1; -.
PIR; PH0872; PH0872.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             119 AA; 12981 MW; 12A709A75344D024 CRC64;
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                                                                                                                                                                                                                                          21-JJJ-1986 (Rel. 01, Created)
21-JJJ-1986 (Rel. 01, Last sequence update)
05-JJJ-2004 (Rel. 44, Last annotation update)
Ig heavy chain VIII region BUR.
Homo sapiens (Human).
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                                                 51 ISNDGSNKFYADSVKG 66
                       2 ISYDGSKKYYADSVKG 17
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nes 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                    HV3L_HUMAN
AC 21-JUL-1986
DT 21-JUL-1986
DT 21-JUL-1986
DE 19 heavy cha
OS Homo saptens
OC Warmania; Bu
OC Mammalia; Bu
OC Mammalia; Bu
OC MELTAXID=9
RN MEDLINE=7915
RA MEDLINE=7915
RA "Primary Btv.,
RT "Primar
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Gaps

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O9ULB6

ઠે 셤 Hypothetical protein.

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TISSUB-Primary B-Cells,

XX Equaberge Ruch, Reingold B.A., Grouse L.H., Derge JG.

A Strauberg R.L., Feingold B.A., Grouse L.H., Derge JG.,

A Strauberg R.L., Feingold B.A., Grouse L.H., Derge JG.,

A Itschul S.F., Zeeberg B., Buscher L., Schaefer C.F., Bhat N.K.,

A Itschul S.F., Zeeberg B., Buscher T., Schaefer C.F., Bhat N.K.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Richards S.A., McEwan P.J., McKernan K.J., Abramson R.D., Mullahy S.J.,

A Robards S.A., McEwan P.J., McKernan K.J., Abramson R.D., Mullahy S.J.,

A Richards S.A., Woley W.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Willalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

A Halakeley R.W., Touchman J.W., Gareen B.D., Dickson M.C.,

A Mitting M. M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

A Mitting M. J., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

A Jones S.J., Marra M.A.;

A Gores S.J., Marra M.A.;

R and mouse CDNA sequences.
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                Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO18147; AAH18747.1; -.
R HSSP; PO1861; 1ADQ.
R InterPro; IPR007110; Ig-1ike.
R InterPro; IPR007110; Ig-1ike.
R InterPro; IPR007359; Ig cl.
R InterPro; IPR003506; Ig W.
R Pfam; PF07654; Cl. 18e0; 3.
R SWART; SM00409; IG; 2.
R SWART; SM00409; IG; 2.
R SWART; SM00409; IG; 1.
R PROSITE; PS50835; IG LIKE; 4.
R PROSITE; PS50835; IG LIKE; 4.
R PROSITE; PS50839; IG MHC; UNKNOWN_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           72.7%; Score 64; DB 2; Length 470; 75.0%; Pred. No. 0.05; 1. Mismatches 3; Indels
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SEQUENCE 470 AA; 51715 MW; 7B49556AllFD7D99 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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Matches 12; Conservative
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                                                                                                                     SEOUENCE FROM N.A.
                                                                           NCBI_TaxID=9606;
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Search completed: October 14, 2005, 16:19:51 Job time : 115.156 secs

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US-09-383-667-18
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Sequence 16, Appl
Sequence 20, Appl
Sequence 36, Appl
Sequence 97, Appl
Sequence 118, App
Sequence 118, App
Sequence 111, App
Sequence 115, App
Sequence 115, App
Sequence 46, Appl
Sequence 46, Appl
Sequence 46, Appl
Sequence 35, Appl
Sequence 35, Appl
Sequence 36, Appl
Sequence 6, Appl
Sequence 96, Appl
Sequence 96, Appl
Sequence 96, Appl
Sequence 96, Appl
Sequence 11, Appl
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                                                                October 14, 2005, 16:00:04; Search time 33.4688 Seconds (without alignments) 37.917 Million cell updates/sec
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1. /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

2. /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

3. /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

3. /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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US-09-383-667-18
US-09-383-667-20
US-09-424-8408-95
US-09-424-8408-95
US-09-424-8408-95
US-09-424-8408-95
US-08-211-202-141
US-08-211-202-141
US-08-211-202-141
US-08-211-202-141
US-08-311-398-46
US-08-311-398-46
US-08-311-202-135
US-08-91-96-46
US-08-91-96-96
US-09-424-8408-77
US-09-424-8408-77
US-09-424-8408-11
                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                     513545 segs, 74649064 residues
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Maximum Match 100%
Listing first 45 summaries
                                              - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                         1 IISYDGSKKYYADSVKG 17
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Maximum DB seq length: 200000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Adams. Camelia W.
APPLICANT: Adams. Camelia W.
APPLICANT: Baron, Dan L.
APPLICANT: Baron, Dan L.
APPLICANT: Baron, Dan L.
APPLICANT: Has, Philip E.
APPLICANT: Judice, J. Kevin
APPLICANT: Gugget, Shelley
TILLE REPRENCE: Ple61R2
TILLE REPRENCE: Ple61R2
CURRENT FILING DATE: 1999-08-26
EARLIER APPLICATION NUMBER: US 60/098,233
EARLIER APPLICATION NUMBER: US 60/098,233
EARLIER PILING DATE: 1999-03-28
EARLIER PILING DATE: 1999-03-3
NUMBER OF EQ ID NOS: 32
SEQ ID NO 11
LENGTH: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 18 Application US/09383667
; Patent No. 6624295
; GENERAL INPORMATION:
; APPLICANT: Adams, Camelia W.
; APPLICANT: Baton, Dan L.
; APPLICANT: Baton, Dan L.
; APPLICANT: Judice, J. Kevin
; APPLICANT: Judice, J. Kevin
; APPLICANT: Suggett, Daniel
; APPLICANT: Suggett, Shelley
; TITLE OF INVENTION: Human Anti-Factor IX/IXa Antibodies
; FILE REFERENCE: P1661R2
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US-09-456-090A-102
US-09-456-090A-108
US-09-455-090A-110
US-09-453-234-108
US-09-453-234-110
US-08-862-124-17
US-08-862-124-14
US-09-560-198A-12
US-09-424-840B-113
US-09-560-198A-2
US-09-560-198A-2
US-09-560-198A-10
US-09-560-198A-10
US-09-560-198A-10
US-09-424-840B-12
US-09-424-840B-2
US-09-424-840B-2
US-09-424-840B-2
US-08-260-198A-10
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Pred. No. 8.1e-07;
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Sequence 20, Application US/09383667

Sequence 20, Application US/09383667

Septent No. 6624295

GENERAL INFORMATION:

APPLICANT: Adams, Camelia W.

APPLICANT: Eaton, Dan L.

APPLICANT: Haston, Dan L.

APPLICANT: Haston, Dan L.

APPLICANT: Aldice, J. Kevin

APPLICANT: Xirchhofer, Daniel

APPLICANT: Suggett, Shelley

TITLE OF INVENTION: Human Anti-Factor IX/IXa Antibodies
                                                                                                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Adams, Camelia W.
APPLICANT: Devaux, Brigitte
APPLICANT: Baron, Dan L.
APPLICANT: Judice, J. Kevin
APPLICANT: Vidice, J. Kevin
APPLICANT: Kirchofer, Daniel
APPLICANT: Suggett, Shelley
TITLE OF INVENTION: Human Anti-Factor IX/IXa Antibodies
FILE REFERENCE: P1661R2
CURKENT FILING DATE: 1999-08-26; EARLIER APPLICATION NUMBER: US 60/098, 233; EARLIER FILING DATE: 1998-08-28; EARLIER PLICATION NUMBER: US 60/122,767; RABLIER FILING DATE: 1999-03-03; NUMBER OF SEQ ID NOS: 32; SEQ ID NO 18; SEQ ID NO 18
                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
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CURRENT FILING DATE: 1999-08-26
EARLIER APPLICATION NUMBER: US 60/098,233
EARLIER FILING DATE: 1998-08-28
EARLIER APPLICATION NUMBER: US 60/122,767
EARLIER APPLICATION NUMBER: US 60/122,767
SEQ ID NO 16
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CURRENT APPLICATION NUMBER: US/09/383,667
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Patent No. 6624295
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                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 94.1%;
Matches 16; Conservative
                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-383-667-18
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-383-667-16
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APPLICANT: Berchcold, Peter

APPLICANT: Berchcold, Peter

TITLE OF INVENTION: ANTI-GPIBA/IIIA RECOMBINANT ANTIBODIES

FILE REFERENCE: 100564-09049

CURRENT APPLICATION NUMBER: US/09/424,840B

CURRENT FILING DATE: 1999-12-03

PRIOR APPLICATION NUMBER: DE 19820663.1

PRIOR APPLICATION NUMBER: DE 19755227.7

PRIOR APPLICATION NUMBER: DE 1975527.7

PRIOR PILING DATE: 1997-12-12

PRIOR PILING DATE: 1997-12-12

PRIOR PILING DATE: 1997-06-06

NUMBER OF SEQ ID NOS: 128

SOFTWARE: PACENTIN VERBION 3.1

EENGTH: 17
                                                                                                                                                                                                                                                                                                              Score 82; DB 4; Length 17;
Pred. No. 1.2e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 17;
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APPLICANT: Berchtold, Peter
APPLICANT: Escher, Robert F. A.
TITLE OF INVENTION: ANTI-GPIB/IIIA RECOMBINANT ANTIBODIES
FILE REFERENCE: 100564-09049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/424,840B
CURRENT FILING DATE: 1999-12-03
PRIOR APPLICATION NUMBER: UB 19820663.1
PRIOR FILING DATE: 1998-05-08
PRIOR FILING DATE: 1997-12-12
PRIOR PILING DATE: 1997-12-12
PRIOR PILING DATE: 1997-12-12
PRIOR FILING DATE: 1997-12-12
PRIOR FILING DATE: 1997-06-06
NUMBER OF SEQ ID NOS: 128
                                                                                                                                                                                                                                                                                                                                                                   Mismatches
CURRENT FILING DATE: 1999-08-26
EARLIER APPLICATION NUMBER: US 60/098,233
EARLIER FILING DATE: 1998-08-28
EARLIER APPLICATION NUMBER: US 60/122,767
EARLIER FILING DATE: 1999-03-03
NUMBER OF SEQ ID NOS: 32
SEQ ID NO 20
LENGTH: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 36, Application US/09424840B; Patent No. 6790938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-424-840B-95; Sequence 95, Application US/09424840B; Patent No. 6790938
                                                                                                                                                                                                                                                                                                              Query Match
93.2%; Soc
Best Local Similarity 100.0%; Pi
Matches 16; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 IISYDGSKKYYADSVK 16
                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-383-667-20
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US-09-424-840B-36
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Sequence 118, Application US/08211202
Sequence 118, Application US/08211202
Fatent No. 556532
GENERAL INFORMATION:
APPLICANT: HOCGENBOOM, Hendricus Renerus Jacobus Matteus
APPLICANT: HOCGENBOOM, Hendricus Renerus Jacobus Matteus
APPLICANT: MINTER, Gregory Faul
TITLE OF INVENTION: Combinatorial approach
TITLE OF INVENTION: Combinatorial approach
TITLE OF INVENTION: Combinatorial approach
CORRESPONDENCE ADDRESS:
ADDRESSEE: David W. Clough, Marshall O'Toole Gerstein Murray &
ADDRESSEE: Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
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                                     Length 17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (BPO)
CURRENT APPLICATION DATA:
APPLICATION INMBER: US/08/211,202
FILING DATE: 23-SEP-1992
                                     Score 82; DB 4; I
Pred. No. 1.2e-06;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 82; DB 1; 1
Pred. No. 7.3e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
PRIOR APPLICATION DATE:
APPLICATION NUMBER: GB 9206372.6
FILING DATE: 24-MAR-1992
RICH APPLICATION NUMBER: PCT/GB92/00883
FILING DATE: 15-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: David W. Clough
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28111/31960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36,107
FR: 28111/31960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 23-SEP-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 68 9120252.3
FILING DATE: 23-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 68 9120377.8
FILING DATE: 25-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 68 9206318.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 118:
SEQUENCE CHARACTERISTICS:
' LENGTH: 98 amino acide
                                                                                                                    1 IISYDGSKKYYADSVKG 17
                                                                                                                                           1 VISYDGSNKYYADSVKG 17
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TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
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                                   Query Match 93.2%;
Best Local Similarity 88.2%;
Matches 15; Conservative
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Best Local Similarity
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ZIP: 60606-6402
  US-09-424-840B-108
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APPLICANT: Berchtold, Peter
APPLICANT: Berchtold, Peter
Becher, Robert F. A.
TITLE OF INVENTION: ANTI-GPIIB/IIIA RECOMBINANT ANTIBODIES
FILE REPRENCE: 100564-09049
CURRENT APPLICATION NUMBER: US/09/424,840B
CURRENT PILING DATE: 1999-12-03
PRIOR APPLICATION NUMBER: DE 1982663.1
PRIOR PILING DATE: 1997-12-12
PRIOR APPLICATION NUMBER: DE 19755227.7
PRIOR APPLICATION NUMBER: DE 19755227.7
PRIOR APPLICATION NUMBER: DE 197552304.8
PRIOR APPLICATION NUMBER: DE 197552304.8
NUMBER OF SEQ ID NOS: 128
SOFTWARE: PATENTIN VETSION 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 93.2%; Score 82; DB 4; Length 17; Best Local Similarity 88.2%; Pred. No. 1.2e-06; Matches 15; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93.2%; Score 82; DB 4; Length 17;
88.2%; Pred. No. 1.2e-06;
tive 1; Mismatches 1; Indels
                                                                                                                                                                           1; Mismatches
                                                                                                                                                                                                                                                                                                                                                          ; Sequence 97, Application US/09424840B; Patent No. 6790938; GENERAL INFORMATION:
                                                                                                                                                                                                                                         1 VISYDGSNKYYADSVKG 17
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 95
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ORGANISM: Homo sapiens
                                                      TYPE: PRT
CRGANISM: Homo sapiens
US-09-424-840B-95
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ORGANISM: Homo sapiens
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Matches 15; Conserva
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                        APPLICANT:
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APPLICANT: Holliger, Kasper
APPLICANT: Holliger, Kasper
APPLICANT: Chiseson, Timochy
APPLICANT: Clackson, Timochy
APPLICANT: Chiseson, Timochy
APPLICANT: Chiseson, Timochy
APPLICANT: Winter, Gregory
APPLICANT: Bonert, Timochy
APPLICANT: 23839-00013
CURRENT APPLICATION NUMBER: US/09/726,219A
CURRENT APPLICATION NUMBER: GB 9015198.6
PRIOR APPLICATION NUMBER: GB 9015198.6
PRIOR PILING DATE: 1990-10-19
PRIOR PILING DATE: 1990-10-19
PRIOR PILING DATE: 1990-11-12
PRIOR APPLICATION NUMBER: GB 9104744.9
PRIOR APPLICATION NUMBER: GB 9104744.9
PRIOR APPLICATION NUMBER: GB 910549.4
PRIOR PILING DATE: 1991-05-15
PRIOR PILING DATE: 1991-05-15
PRIOR PILING DATE: 1991-07-10
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US-08-211-202-141
; Sequence 141, Application US/08211202
; Patent No. 5565332
; GENERAL INFORMATION:
; APPLICANT: HOOGENBOOM, Hendricus Renerus Jacobus Matteus
; APPLICANT: BAIER, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93.2%; Score 82; DB 4; Length 115; 88.2%; Pred. No. 8.6e-06;
  1; Indels
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APPLICANT: Cambridge Antibody Technology Limited
APPLICANT: Medical Research Council
APPLICANT: McCafferty, John
APPLICANT: Pope, Anthony
  1; Mismatches
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PRIOR FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 272
SOFTWARE: PatentIn version 3.1
SEQ ID NO 167
LENGTH: 115
                                                                                                                                                                                                              Sequence 167, Application US/09726219A
Patent No. 6806079
                                                                                                                                                                                                                                                                                                                                                                                                  Johnson, Kevin
Hoogenboom, Hendricus
Griffiths, Andrew
                                              1 IISYDGSKKYYADSVKG 17
                                                                           50 VISYDGSNKYYADSVKG 66
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  15; Conservative
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; ORGANISM: Homo sapiens
US-09-726-219A-167
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Matches 15; Conserv
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US-09-726-219A-167
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Matches
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Gaps
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US-08-545-809A-115
US-08-6056B7B
Sequence 115, Application US/08545809A
Patent No. 6056B7B
GENERAL INFORMATION:
APPLICANT: Honjo, Tasuku
TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
TUTLE OF INVENTION: 145
CORRESPONDENCE ADDRESS:
                                    TITLE OF INVENTION: TECHNICAL CHIMERIC ANTIDODIES - A
TITLE OF INVENTION: Combinatorial approach
NUMBER OF SEQUENCES: 144
CORRESPONDENCE ADDRESS:
ADDRESSEE: David W. Clough, Marshall O'Toole Gerstein Murray &
ADDRESSEE: Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STAFE: Illinois
COUNTRY: USA
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MEDIUM TYE: BOOGO 402

COMPUTER READABLE FORM:

MEDIUM TYER: Floppy disk

COMPUTER: READABLE FORM:

MEDIUM TYER: FLOPPy disk

COMPUTER: READABLE FORM:

MEDIUM TYER: FLOPPy disk

COMPUTER: Decentin Release #1.0, Version #1.25 (EPO)

SOFTWARE: Pacentin Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: GB 912025.3

FRIOR APPLICATION NUMBER: GB 912037.8

FILING DATE: 23-SEP-1991

APPLICATION NUMBER: GB 9206318.9

FILING DATE: 24-MAR-1992

PRIOR APPLICATION NUMBER: GB 9206318.9

FILING DATE: 24-MAR-1992

PRIOR APPLICATION NUMBER: GB 9206372.6

FILING DATE: 24-MAR-1992

PRIOR APPLICATION NUMBER: GB 9206372.6

FILING DATE: 24-MAR-1992

APPLICATION NUMBER: PCT/GB92/00883

FILING DATE: 14-MAR-1992

APPLICATION NUMBER: PCT/GB92/00883

FILING DATE: 15-MAR-1992

ATTORNEY/AGENT INFORMATION:

NUMBE: DAVIG M. CLOUGH

NUMBER: DAVIG M. CLOUGH

NUMBER: DAVIG M. CLOUGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
                      Gregory Paul Production of chimeric antibodies combinatorial approach
Stephane Anne Therese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 93.2%; Score 82; DB 1; I
Best Local Similarity 88.2%; Pred. No. 8.7e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: David W. Clough
REGISTRATION NUMBER: 36,107
REPERNICE/DOCKET NUMBER: 28111/31960
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
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US-08-131-3978-46

Sequence 46, Application US/08331397B

Patent No. 5891726

Patent No. 5891726

Patent No. 5891726

APPLICANT Paten, Ital

TITLE OF INVENTION: Chimeric and Mutationally Stabilized Tumor-
TITLE OF INVENTION: Chimeric and Mutationally Stabilized Tumor-
TITLE OF INVENTION: Specific Antibody Pragments, Pusion Proteins, and Uses

TITLE OF INVENTION: These of

TELECHONE: TELECOPHURE: 12-CCT-1994

TELECOPHURICATION NUMBER: 30-58P-1991

PROCKET NUMBER: 30-58P-1991

PROCKET NUMBER: 30-58P-1991

PROCKET NUMBER: 30-58P-1991

TELECOPHURICATION NUMBER: 30-498

RESERVENCE OF CONTENTION: THORWATION:

TELECOPHURE: TELECOPHURE: 1455-39-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 93.2%; Score 82; DB 1; Length 119; Best Local Similarity 88.2%; Pred. No. 8.9e-06; Matches 15; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: Protein
LOCATION: 1..19
OTHER INDORATION:
OTHER INFORMATION: 56P1'CL Variable Heavy chain (V-H)"
                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/596,289
FILING DATE: 12-0CT-1990
ATTORNEY/AGENT INFORMATION:
NAME: HUNTER, TOM
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 015280-126110US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEPHONE: (415) 543-5043
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 119 amino acide
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
       30-SEP-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-331-398A-46
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APPLICANT: Willingham, Mark
APPLICANT: Willingham, Mark
APPLICANT: FitzGerald, David
APPLICANT: FitzGerald, David
APPLICANT: FitzGerald, David
APPLICANT: Pai, Lee
TITLE OF INVENTION: Single Chain B3 Antibody Fusion Proteins
TITLE OF INVENTION: and Their Uses (as amended)
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Street Plaza
CITY: San Francisco
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COMPUTER READABLE FORM:

MEDIUM TYPE: RADAPY disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/NS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/331,398A

FILING DATE: 28-OCT-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/767,331
                                                                                                                                                           COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: I based the
COMPUTER: I based the
COMPUTER: Diskette
COMPUTER: DIskett
ADDRESSEE: Fish & Richardson, P.C. STREET: 225 Franklin Street CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 46, Application US/08331398A Patent No. 5608039 GENERAL INFORMATION:
APPLICANT: Paten, Ira APPLICANT: Willingham, Mark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 IISYDGSKKYYADSVKG 17
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Best Local Similarity 88.27
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MOLECULE TYPE: protein
                                                                                                                                            RY: US
02110-2804
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STATE: Califor
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-545-809A-115
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                                                                         CITY: BOE
STATE: MA
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ઠ
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Gaps

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STRANDEDNESS
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; Sequence 46, Application US/08759804A
; Patent No. 5990296
; GENERAL INFORMATION:
    APPLICANT: Pastan, Ira
    APPLICANT: FitzGerald, David J.
    APPLICANT: Brinkmann, Ulrich
    APPLICANT: Pair Lee
    TITLE OF INVENTION: Tumor-Specific Antibody Fragments,
    TITLE OF INVENTION: Fusion Proteins, and Uses Thereof
    NUMBER OF SEQUENCES: 68
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: Townsend and Townsend and Crew LLP
    STREET: Two Embarcadero Center, Eighth Floor
    CITY: San Francisco
    STATE: California
    COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                               Query Match 93.2%; Score 82; DB 2; Length 119; Best Local Similarity 88.2%; Pred. No. 8.9e-06; Matches 15; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                  NAME/KEY: Protein

1.00ATION: 1.119

OTHER INFORMATION: /note= "Human fetal immunoglobulin office information: 56Pl'CL Variable Heavy chain (V-H)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCUNTRY: USA
ZIF: 94111-3834
COMPUTER RELABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-006/Ms-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 08/331,398
FILING DATE: 03-DEC-1996
CLASSIFICATION NUMBER: US 08/331,398
FILING DATE: 28-OCT-1994
PRIOR APPLICATION NUMBER: US 07/767,331
PRIOR APPLICATION NUMBER: US 07/767,331
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/767,331
FILING DATE: 12-OCT-1990
ATTORNEY/AGENT INFORMATION:
PRIOR APPLICATION NUMBER: 32,762
ATTORNEY/AGENT INFORMATION:
TELEPHONE: (415) 576-0300
TELEFRAL (415) 576-0300
TELEFRAL (415) 576-0300
TUPORMATION POR SEO ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acids
TYPE: amino acids
TELEFAX: (415) 543-5043
INFORMATION FOR END ID NO: 46: SEQUENCE CHARACTERISTICS: LENGTH: 119 amino acids TYPE: amino acid STRANDEDNESS: TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 IISYDGSKKYYADSVKG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50 VISYDGSNKYYADSVKG 66
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US-08-759-804A-46
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TOPOLOGY: linear

MOLECTLE TYPE: protein

FRATURE:
NAME/KEY: Protein

LOCATION: 1..119

OTHER INFORMATION: 56P1'CL Variable Heavy chain (V-H)"

US-08-759-804A-46

Query Match

Sest Local Similarity 88.2%; Pred. No. 8.9e-06;

Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps

Oy 1 IISYDGSKKYYADSVKG 17

Cy 1 IISYDGSKKYYADSVKG 17

Search completed: October 14, 2005, 16:22:00

JOb time : 33.4688 secs
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Sequence 262, App
Sequence 914, App
Sequence 1323, Ap
Sequence 914, App
Sequence 914, App
Sequence 1323, Ap
Sequence 1114, Ap
Sequence 1114, Ap
Sequence 1114, Ap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                      October 14, 2005, 16:20:10 ; Search time 120.859 Seconds (without alignments) 58.615 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Published Applications AA:*

1: \cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
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10: \cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-989-462-362
US-09-880-748-914
US-09-880-748-1323
US-10-293-418-1323
US-10-293-418-1323
US-10-293-418-1323
US-10-293-418-1323
US-10-293-418-1314
US-10-293-418-1114
US-10-989-462-276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                 - protein search, using sw model
                                                                                                                                                                                                                                                                                       BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match
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                                                                                                                                                                                                                               Perfect score:
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No.
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12 86 97.7 135 15 US-10-364-743-97 Sequence 97, Appl 14 84 95.5 117 17 US-10-630-009-24 Sequence 24, Appl 15 US-09-228-708-24 Sequence 24, Appl 16 US-09-228-708-10 Sequence 10, Appl 17 US-10-630-009-10 Sequence 10, Appl 18 95.5 101 17 US-10-630-009-10 Sequence 10, Appl 19 95.5 101 17 US-10-630-009-10 Sequence 10, Appl 19 95.5 101 17 US-10-630-009-10 Sequence 10, Appl 19 94.3 122 10 US-10-20-208-98 Sequence 10, Appl 20 94.3 122 12 US-10-20-727-155-14 Sequence 58, Appl 20 94.3 137 15 US-10-364-743-11 Sequence 58, Appl 20 94.3 137 15 US-10-364-743-19 Sequence 11, Appl 20 94.3 137 15 US-10-364-743-19 Sequence 11, Appl 20 94.3 137 15 US-10-452-593-11 Sequence 1690, Appl 20 94.3 137 15 US-10-452-593-19 Sequence 1690, Appl 20 94.3 137 15 US-10-452-593-19 Sequence 1690, Appl 20 94.3 137 15 US-10-99-80-748-1690 Sequence 1690, Appl 20 94.3 137 15 US-10-394-999 Sequence 1690, Appl 20 94.3 137 15 US-10-394-999 Sequence 1690, Appl 20 94.3 137 15 US-10-394-991-999 Sequence 67, Appl 20 94.3 137 15 US-10-394-999 Sequence 67, Appl 20 94.3 17 15 US-10-394-999 Sequence 67, Appl 20 94.3 17 15 US-10-394-999 Sequence 67, Appl 20 94.3 17 15 US-10-394-999 Sequence 97, Appl 20 94.3 17 16 US-10-394-999 Sequence 97, Appl 20 94.3 17 17 18 US-10-394-999 Sequence 97, Appl 20 94.3 17 17 18 US-10-394-999 Sequence 97, Appl 20 94.3 17 17 18 US-10-394-999 Sequence 97, Appl 20 94.3 17 18 US-10-394-999 Sequence 97, Appl 20 94.3 17 17 US-10-394-999 Sequence 97, Appl 20 94.3 17 10 US-10-394-999 Sequence 97, Appl 20 94.3 17 17 US-10-394-999 Sequence 97, Appl 20 94.3 17 17 US-10-394-999 Sequence 97, Appl 20 94.3 17 17 US-10-394-999 Sequence 97, Appl 20 94.3 17 18 US-10-394-999 Sequence 97, Appl 20 94.3 17 18 US-10-394-999 Sequence 97, Appl 20 94.3 17 18 US-11-074-804-999 Sequence 97, Appl 20 94.3 17 18 US-11-074-804-999 Seque
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RESULT 1

US-10-989-462-300

US-10-989-462-300

US-10-989-462-300

Sequence 300, Application US/10989462

Publication NO. US20050220795A1

GENERAL INFORMATION:

APPLICANT: Wittrup, K. Dane

APPLICANT: Wittrup, K. Dane

APPLICANT: Wittrup, ANTI-HYDROXYLASE ANTIBODIES AND USES

TITLE OF INVENTION: ANTI-HYDROXYLASE ANTIBODIES AND USES

TITLE OF INVENTION: THEREOF

CURRENT FILING DATE: 2004-11-15

CURRENT FILING DATE: 2003-11-14

PRIOR APPLICATION NUMBER: US 60/520,114

PRIOR APPLICATION NUMBER: US 60/520,114

PRIOR PILING DATE: 2003-11-14

PRIOR FILING DATE: 2003-11-14

PRIOR FILING DATE: 2004-04-19

NUMBER OF SEQ ID NOS: 319

SOFTWARE: FactSEQ for Windows Version 4.0

SEQ ID NO 300

CONGANISM: Artificial Sequence

FEATURE:

FEATURE:

PRIOR FILING DATE: 2004-04-19

NUMBER OF SEQ ID NOS: 319

SOFTWARE: PAT

ORGANISM: Artificial Sequence

FEATURE:

PATURE:

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; Publication No. US20030059937A1
GENERAL INPORMATION:
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
; FILE REFERENCE: PF23
; CURRENT PLING DATE: 2001-06-15
; PRIOR PILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR PLING DATE: 2000-06-15
; PRIOR PLING DATE: 2000-06-15
; PRIOR FILING DATE: 2000-10-17
; PRIOR FILING DATE: 2000-10-17
; PRIOR FILING DATE: 2001-03-16
; PRIOR FILING DATE: 2001-03-16
; PRIOR FILING DATE: 2001-03-21
; SOFTWARE: PALENTING NUMBER: 60/293,499
; SOFTWARE: PALENTING NUMBER: 2001-03-21
; BRIOR FILING DATE: 2001-03-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 121;
                                   Sequence 262, Application US/10989462
; Sequence 262, Application US/10989462
; Publication No. US20050220795A1
; GENERAL INFORMATION:
   APPLICANT: Wittrup, K. Dane
; APPLICANT: Wittrup, K. Dane
; TITLE OF INVENTION: THEREOF
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 01997-329001
; CURRENT APPLICATION NUMBER: US/10/989,462
; CURRENT PILING DATE: 2004-11-15
; PRIOR PELICATION NUMBER: US 60/520,114
; PRIOR PLICATION NUMBER: US 60/520,114
; PRIOR PLICATION NUMBER: US 60/53,514
; PRIOR PLING DATE: 2003-11-14
; PRIOR PLING DATE: 2004-04-19
; NUMBER OF SEQ ID NOS: 319
; SOFTWARE: FREESEQ for Windows Version 4.0
; SEQ ID NO 262
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Best Local Similarity 94.1%; Pred. No. 1.2e-05;
Matches 16; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Synthetically generated peptide
US-10-989-462-262
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US-09-880-748-914
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                                US-10-989-462-262
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50 VISYDGSKKYYADSVKG 66

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ) General invocation.
) General invocation.
) TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

PRICE PESSON

CURRENT APPLICATION NUMBER: US/09/880,748

CURRENT PILING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR PILING DATE: 2000-61-15

PRIOR PILING DATE: 2000-10-17

PRIOR PILING DATE: 2001-03-16

PRIOR PILING DATE: 2001-03-16

PRIOR PILING DATE: 2001-03-21

PRIOR PILING DATE: 2001-03-21

PRIOR PILING DATE: 2001-05-25

NUMBER OF SEQ ID NOS: 3239

SOFTWARE: Patentin Ver. 2.0

ENDOR PILING DATE: 2001-05-25

NUMBER OF SEQ ID NOS: 3239

SOFTWARE: Patentin Ver. 2.0
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Pred. No. 2.5e-05;
1; Mismatches 0; Indel8
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ilarity 94.1%; Pred. No. 2.5e-05;
Conservative 1; Mismatches 0;
Sequence 916, Application US/09880748
Publication No. US20030059937A1
GENERAL INFORMATION:
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Best Local Similarity 94.1%;
Matches 16; Conservative
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US-09-880-748-916
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Best Local Similarity
Matches 16; Conserv?
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US-09-880-748-1323
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Gaps
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Publication No. US20030223996A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REFERENCE: PF523P2

CURRENT APPLICATION NUMBER: US/10/293,418

CURRENT FILING DATE: 2001-11-27

PRIOR APPLICATION NUMBER: 60/331,469

PRIOR FILING DATE: 2001-11-16

PRIOR PRIOR PELING DATE: 2001-12-19

PRIOR FILING DATE: 2001-12-19

PRIOR FILING DATE: 2001-0-15

PRIOR PRIOR PRILING DATE: 2001-0-15

PRIOR PRILING DATE: 2001-0-12

PRIOR PRILING DATE: 2001-0-12

PRIOR PRILING DATE: 2001-0-12

PRIOR APPLICATION NUMBER: 60/270,249

PRIOR FILING DATE: 2001-0-12

PRIOR APPLICATION NUMBER: 60/270,248

PRIOR FILING DATE: 2001-0-12

PRIOR APPLICATION NUMBER: 60/210,210

PRIOR FILING DATE: 2001-0-17

PRIOR FILING DATE: 2001-0-17

PRIOR FILING DATE: 2001-0-17

PRIOR FILING DATE: 2000-06-16

NUMBER OF SEQ ID NOS: 3247

LENGTH. 248
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Publication No. US20030059937A1

GENERAL INFORMATION:

APPLICATION NO. US20030059937A1

GENERAL INFORMATION:

ATILE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REFREENCE: PFS23

CURRENT FILING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR PLING DATE: 2000-6-15

PRIOR PLING DATE: 2000-6-15

PRIOR PELICATION NUMBER: 60/240,816

PRIOR PELICATION NUMBER: 60/240,816

PRIOR PELICATION NUMBER: 60/240,816

PRIOR PILING DATE: 2000-10-16

PRIOR FILING DATE: 2000-10-16
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                                                                           Score 87; DB 15; Length 248;
Pred. No. 2.5e-05;
1; Mismatches 0; Indels
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Pred. No. 2.5e-05;
1; Mismatches 0; Indels
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FILING DATE: 2001-03-21
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PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
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Best Local Similarity 94.1%;
Matches 16; Conservative
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Best Local Similarity 94.1%;
Matches 16; Conservative
; ORGANISM: Homo sapiens
US-10-293-418-916
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US-10-293-418-1323
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US-10-293-418-1323
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Sequence 916, Application Wo. US20030223996A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.

ITILE OF INVENTION:

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REFERENCE: PF523P2

CURRENT FILING DATE: 2002-11-27

PRIOR APPLICATION NUMBER: 06/331,469

PRIOR PILING DATE: 2001-11-16

PRIOR PILING DATE: 2001-11-19

PRIOR PELING DATE: 2001-05-15

PRIOR PELING DATE: 2001-06-15

PRIOR PELING DATE: 2001-01-03-21

PRIOR PELING DATE: 2001-03-21

PRIOR PELING DATE: 2000-10-17

PRIOR PELING DATE: 2000-10-17

PRIOR PELING DATE: 2000-06-16

NUMBER OF SEQ ID NOS: 3247

LENGTH: 248

LENGTH: 248

LENGTH: 248
                                                               Sequence 914, Application US/10293418
Publication No. US20030223996A1
GENERAL INFORMATION:
APPELICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF523P2
CURRENT APPLICATION NUMBER: US/10/293,418
CURRENT FILING DATE: 2002-11-27
PRIOR PILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR FILING DATE: 2001-12-19
PRIOR FILING DATE: 2001-06-15
PRIOR PRIOR DATE: 2001-06-15
PRIOR PLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-06-15
PRIOR FILING DATE: 2001-06-15
PRIOR PILING DATE: 2001-03-21
PRIOR PILING DATE: 2001-03-21
PRIOR PILING DATE: 2001-03-21
PRIOR PILING DATE: 2000-10-3-1
PRIOR PILING DATE: 2000-10-17
PRIOR PILING DATE: 2000-06-16
NUMBER OF SEQ ID NOS: 3247
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 16; Conserv
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ORGANISM: human
US-10-364-743-97
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JUNEARL INVOLVILLON:

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF523P2
CURRENT APPLICATION NUMBER: US/10/293,418
CURRENT FILING DATE: 2002-11-27
PRIOR APPLICATION NUMBER: 60/314,469
PRIOR PELING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/314,817
PRIOR PELING DATE: 2001-12-19
PRIOR PILING DATE: 2001-12-19
PRIOR PILING DATE: 2001-63-15
PRIOR PLING DATE: 2001-06-15
PRIOR PLING DATE: 2001-06-15
PRIOR PLING DATE: 2001-03-21
PRIOR PLING DATE: 2001-03-21
PRIOR PLING DATE: 2001-03-16
PRIOR PLING DATE: 2001-01-16
PRIOR PLING DATE: 2001-01-16
PRIOR PLING DATE: 2000-10-16
PRIOR PLING DATE: 2000-10-16
PRIOR FILING DATE: 2000-10-17
PRIOR FILING DATE: 2000-10-17
PRIOR FILING DATE: 2000-10-17
PRIOR FILING DATE: 2000-10-17
PRIOR FILING DATE: 2000-616
PRIOR PLING DATE: 2000-10-17
PRIOR PLING DATE: 2000-616
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR PLING DATE: 2000-10-17
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Publication No. US20050220795A1
GENERAL INFORMATION.
APPLICANT: Wittrup, K. Dane
APPLICANT: Yeung, Yik Andy
APPLICANT: Yeung, Yik Andy
APPLICANT: Yeung, Yik Andy
APPLICANT: Yeung, Yik Andy
APPLICANTION: ANTI-HYPROXYLASE ANTIBODIES AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 01997-329001
CURRENT FAPPLICATION NUMBER: US/10/989,462
CURRENT FILING DATE: 2004-11-15
PRIOR APPLICATION NUMBER: US 60/520,114
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Publication No. US20030223996A1
GENERAL INFORMATION:
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PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1114
LENGTH: 251
                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
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US-10-293-418-1114
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US-10-989-462-276
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                                                                                                                                                                                                                                                                                                                                                                Query Match 98.9%; Score 87; DB 18; Length 252; Best Local Similarity 94.1%; Pred. No. 2.5e-05; Matches 16; Conservative 1; Mismatches 0; Indels
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APPLICANT: Wild, Martha A.
APPLICANT: Maruyama, Toshiaki
APPLICANT: Maruyama, Toshiaki
APPLICANT: Maruyama, Toshiaki
APPLICANT: Nolan, Mary Jean
TITLE OF INVENTION: IMMUNOTHERAPEUTICS FOR BIODEFENSE
FILE REFERENCE: 98 CTP (1087-73 CIP)
CURRENT APPLICATION NUMBER: US/10/452,593
CURRENT FILING DATE: 2003-06-02
PRIOR FILING DATE: 2003-02-11
PRIOR APPLICATION NUMBER: US 60/356,086
PRIOR FILING DATE: 2002-02-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Brederickson, Shana
APPLICANT: Frederickson, Shana
APPLICANT: Wild, Martha A.
APPLICANT: Wild, Martha A.
APPLICANT: Wild, Martha A.
APPLICANT: Wo. US20040009178Alan, Mary Jean
APPLICANT: No. US20040009178Alan, Mary Jean
TITLE OP INVENTION: IMMUOTHERAPEUTICS FOR BIODEFENSE
FILE REFERENCE: 84 (1087-73)
CURRENT APPLICATION NUMBER: US/10/364,743
CURRENT FILING DATE: 2003-02-11
PRIOR APPLICATION NUMBER: US 60/428,807
PRIOR APPLICATION NUMBER: US 60/428,807
PRIOR APPLICATION NUMBER: 125
NUMBER OF SEQ ID NOS: 118
SEQ ID NO 97
LENGTH: 135
LENGTH: 135
                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Synthetically generated peptide US-10-989-462-276
PRIOR FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: US 60/563,514
PRIOR FILING DATE: 2004-04-19
NUMBER OF SEQ ID NOS: 319
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 276
LENGTH: 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-452-593-97; Application US/10452593; Sequence 97, Application US/040258699A1; Publication No. US20040258699A1; EBENEAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 97, Application US/10364743; Publication No. US20040009178A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 IISYDGSKKYYADSVKG 17
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                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Artificial Sequence
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Search completed: October 14, 2005, 17:00:42 Job time: 121.859 secs
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APPLICANT: Ditzel, H.
APPLICANT: Button, D.
APPLICANT: Schaller, M.
APPLICANT: Schaller, M.
APPLICANT: Schaller, M.
TITLE OF INVENTION: Autoimmune disease
TITLE OF INVENTION: Autoimmune disease
CURRENT APPLICATION NUMBER: 136.055031
CURRENT APPLICATION NUMBER: 105.0924
CURRENT FILING DATE: 2001-09-24
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 24
LENGTH: 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95.5%; Score 84; DB 9; Length 17; 88.2%; Pred. No. 4.7e-06; Live 2; Mismatches 0; Indels
PRIOR APPLICATION NUMBER: US 60/376,408
PRIOR FILLING DATE: 2002-04-29
PRIOR PILLING DATE: 2002-04-29
PRIOR PILLING DATE: 2002-11-25
NUMBER OF SEQ ID NOS: 118
SOFTWARE: RECORD TO SEQ ID NOS: 118
SEQ ID NO 97
LENGTH: 135
                                                                                                                                                                                                                                                                                                                                                        Sequence 24, Application US/09828708
Patent No. US20020146753A1
                                                                                                                                                                                                                                                  1 IISYDGSKKYYADSVKG 17
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Matches 15, Conservative
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ORGANISM: Homo sapiens
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; ORGANISM: Homo sapiens
US-10-630-009-24
                                                                                                                            TYPE: PRT
ORGANISM: human
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US-09-828-708-24
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US-10-630-009-24
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 Length 17;
                         0; Indels
Score 84; DB 17;
Pred. No. 4.7e-06;
2; Mismatches 0;
                                                                 1 VISYDGNKKYYADSVKG 17
Query Match
Best Local Similarity 88.2%;
Matches 15; Conservative
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5.1.6
Compugen Ltd.
GenCore version (c) 1993 - 2005
           Copyright
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protein - protein search, using sw model Run on: δ

October 14, 2005, 15:51:19; Search time 84.5625 Seconds (without alignments) 50.310 Million cell updates/sec

US-10-614-959-12 50 1 ASIAAARVLDY 11 score: Title: Perfect sc Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2105692 seqs, 386760381 residues Searched:

2105692 Total number of hits satisfying chosen parameters:

08 08

seq length: 0 seq length: 200000000 Minimum I Maximum I

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp1990s:*geneseqp2000s:* A_Geneseq_16Dec04:* 1: geneseqp1980s:* 2: geneseqp1990e:* geneseqp2003as:* geneseqp2003bs:* geneseqp2002s:* geneseqp2004s:* •• Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		lon	Anti-fact		Oil-assoc	Human pol	Bacterial	Bacterial	Bacterial		Listeria	Zea шаув					Arabidops	Sequence		-	Thermitas	Thermitas	•	Thermitas	Thermitas		Thermitas
		Description	79	Aay79077	Adj48827	Aao13448	Ads26132	Ads25655	Ads25373	Ads22602	Abb48560	Aag18510	Aag18509	Aay37904	Ads28058	Aag20306	Aag51887	Aap80850	Aap80274	Aar54838	Aaw00768	Aaw00769	Aaw00774	Aaw00798	Aaw00770	Aaw00775	Aaw00780
SUMMARIES			9070	9077	8827	3448	6132	5655	5373	2602	8560		8509	7904	8058	0306	1887	0850	0274	4838	0768	0769	0774	0798	0770	0775	0780
S		ឧ	AAY79070	AAY79077	ADJ48827	AA013448	ADS26132	ADS25655	ADS25373	ADS22602	ABB48560	AAG18510	AAG18509	AAY37904	ADS28058	AAG20306	AAG51887	AAP80850	AAP80274	AAR54838	AAW00768	AAW00769	AAW00774	AAW00798	AAW00770	AAW00775	AAW00780
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	Query	Match	100.0	92.0	74.0	72.0	72.0	72.0	72.0	72.0	70.0	68.0	68.0	68.0	68.0	68.0	68.0	68.0	68.0	68.0	68.0	68.0	68.0	68.0	68.0	68.0	68.0
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AAW00783 AAW00792 AAW00772	AAW00784 AAW00793 AAW00796	AAW00794 AAW00776 AAW00785	AAW00787 AAW00789 AAW00799	AAW00803 AAW00767	AAW00801 AAW00790	AAW00788 AAW00797 AAW00800
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ALIGNMENTS

Complementarity determining region 3; CDR3; antibody; Gla domain; factor IX/IXa; blood coagulation; deep venous thrombosis; arterial thrombosis; unstable angina; post myocardial infarction; coronary artery bypass graft; CABG; stroke; tumour growth; metastasis; percutaneous transluminal coronary angioplasty; PTCA; inflammation; septic shock; hypotension; adult respiratory distress syndrome; ARDS; arterial fibrillation; disseminated intravascular coagulopathy; DIC. Anti-factor IX/IXa antibody H chain V domain CDR3 amino acid sequence. AAY79070 standard; peptide; 11 AA. (first entry) 12-JUN-2000 AAY79070;

Homo sapiens.

WO200012562-A1.

09-MAR-2000.

99WO-US019453. 26-AUG-1999; 98US-0098233P. 99US-0122767P. 28-AUG-1998; 03-MAR-1999;

(GETH) GENENTECH INC.

Kirchhofer D; Judice JK, Devaux B, Eaton DL, Hass PE, Adams CW, Suggett S;

WPI; 2000-256595/22.

Novel human anti-Factor IX/IXa antibodies against IX/IXa gamma-carboxyglutamic acid domains useful as anti-coagulant in thrombosis, stroke, and post myocardial infarction.

Claim 2; Fig 2; 84pp; English.

This sequence represents a complementarity determining region 3 (CDR3) of the heavy chain variable domain of a human anti-factor IX/IXa Gla domain antibody. Factor IXa is a vitamin K dependent plasma serine protease that participates in the blood coagulation pathways. Na Gla domain of factor IXa and its zymogen factor IX contains important structural determinants for interaction with high affinity binding sites on vascular endothelial

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the treatment or prophylaxis of thrombotic or coagulopathic diseases or disorders in a mammal for which inhibiting a FIX/IXa mediated event is disorders in a mammal for which inhibiting a FIX/IXa mediated event is indicated, e.g. deep venous thrombosis, arterial thrombosis, unstable angina, post myocardial infarction, post surgical thrombosis, coronary artery bypass graft (CABG), percutaneous transluminal coronary angioplasty (FTCA), stroke, tumour growth, invasion or metastasis, inflammation, septic shock, hypotension, adult respiratory distress syndrome (ARDS), arterial fibrillation and disseminated intravascular coagulopathy (DIC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Complementarity determining region 3; CDR3; antibody; Gla domain; factor IX/IXa; blood coagulation; deep venous thrombosis; arterial thrombosis; unstable angina; post myocardial infarction; coronary artery bypass graft; CABG; stroke; tumour growth; metastesis; percutaneous transluminal coronary angioplasty; PTCA; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anti-factor IX/IXa antibody H chain V domain CDR3 amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 septic shock; hypotension; adult respiratory distress syndrome; ARDS; arterial fibrillation; disseminated intravascular coagulopathy; DIC.
                                                                                                                                                                                                                                                                                                 Gaps
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0
                                                                                                                                                                                                                                                              Length 11;
                                                                                                                                                                                                                                                                                                 0; Indels
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                                                                                                                                                                                                                                                            Score 50; DB 3;
Pred. No. 0.003;
Mismatches 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY79077 standard; peptide; 11 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98US-0098233P.
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                                                                                                                                                                                                                                                                            Best Local Similarity 100.
Matches 11; Conservative
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                                                                                                                                                                                                                                                                                                                                       1 ASIAAARVLDY
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                                                                                                                                                                                                                         Sequence 11 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-AUG-1999;
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03-MAR-1999;
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                                                                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel recombinant DNA construct comprising a promoter functional in plants operably linked to an oil-associated gene for producing transgenic
indicated, e.g. deep venous thrombosis, arterial thrombosis, unstable angina, post myocardial infarction, post surgical thrombosis, coronary artery bypass graft (CABG), percutaneous transluminal coronary angioplasty (PTCA), stroke, tumour growth, invasion or metastasis, inflammation, septic shock, hypotension, adult respiratory distress syndrome (ARDS), arterial fibrillation and disseminated intravascular coagulopathy (DIC)
                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                    oil-associated gene; transgenic; enhanced seed oil; vegetable oil.
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                                                                                                                                                    Length 11;
                                                                                                                                                                              1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ledeaux JR,
                                                                                                                                                  Score 46; DB 3;
Pred. No. 0.019;
); Mismatches
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No.
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26-JUN-2002; 2002US-0391786P.
26-JUN-2002; 2002US-0392018P.
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80.0%;
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                                                                                                                                                    92.0%;
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                                                                                                                                                 Query Match
Best Local Similarity 90.9
Matches 10; Conservative
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RAVANELLO M.
SAVAGE T.
LEDEAUX J R.
                                                                                                                                                                                                                                         1 ASIAAGRVLDY
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                                                                                                                        Sequence 11 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            plant seed
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(LEDE/) I
(ROGE/) F
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New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.
                                                                                              Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; construct; trolerance; construct; pathogen tolerance; pathogen tolerance; pathogen tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomannan; bacterial polypeptide.
                                                                     Bacterial polypeptide #15165.
                                                                                                                                                                                                                                                                                                 20-FEB-2003; 2003US-00369493
                                                                                                                                                                                                                                                                                                                             21-FEB-2002; 2002US-0360039P.
                                          02-DEC-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2004-061375/06
                                                                                                                                                                                                                                          US2003233675-A1.
                                                                                                                                                                                                                                                                      18-DEC-2003
                                                                                                                                                                                                              Bacteria.
                ADS26132
                                                                                                                                                                                                                                                                                                                                                         (CAOY/)
                                                                                                                                                                                                                                                                                                                                                                                                                (GOLD/)
                                                                                                                                                                                                                                                                                                                                                                                                                                             Cao Y,
                                                                                                                                                                                                                                                                                                                                                                                    (SLAT/)
                                                                                                                                                                                                                                                                                                                                                                        (HINK/)
                                                                                                                                                                                                                                                                                                                                                                                                    CHEN/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polyneptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, immunomodulatory activity and activity, tissue growth factor activity, immunomodulatory activity and activity, tissue growth factor activity, immunomodulatory activity and activity, including in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukemia, inflammation and immune disorders.
                                                                                                                                                                                                                                          Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopolesis; tissue growth factor; immunomodulatory; cancer; leukaemla; nervous system disorders; arthritis; inflammation.
  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 20; SEQ ID NO 27340; 1399pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 36; DB 4; Length 58;
Pred. No. 12;
2; Mismatches 1; Indels
  Indels
  1;
 Mismatches
                                                                                                                           AA013448 standard; protein; 58 AA.
                                                                                                                                                                                                              Human polypeptide SEQ ID NO 27340.
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70.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                               28-FEB-2000; 2000US-00515126.
18-MAY-2000; 2000US-00577409.
                                                                                                                                                                                                                                                                                                                                                                                                    26-FEB-2001; 2001WO-US004927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fang YT, Liu C, Drmanac RT
                                                                                                                                                                                   (first entry)
 8; Conservative
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275 ASLAAARALD 284
                             10
                          1 ASIAAARVLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-514838/56.
N-PSDB; AAI93379.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 58 AA;
                                                                                                                                                                                                                                                                                                                                            WO200164835-A2.
                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                   06-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                        07-SEP-2001.
                                                                                                                                                        AA013448;
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Matches
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Goldman BS;

Chen X,

Slater SC,

Hinkle GJ,

CAO Y. HINKLE G J. SLATER S C.

GOLDMAN B S

CHEN X.

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The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a cransformed plant having an improved property. The plant is a crop plant such as maize or soybean. The method of producing a transformed plant cauch as maize or soybean. The method of producing a transformed plant cannot be an improved property comprises transforming a plant with the recombinant DNA construct and growing the transformed plant, where the polynucleotide or polypeptide is useful for improving plants with improved plant properties, e.g. improved cold, heat or drought tolerance, colerance to hearbicides, extreme osmotic conditions or drought tolerance, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of content, improved yield by modification of carbohydrate, nitrogen or providing improved plant growth and development under at least one stress condition, improved plant growth and development under at least one stress condition. Improved plant growth and development under at least one stress condition. This sequence represents a bacterial polypeptide used in the scope of the printed specification of publy patent did not form at each ord. The printed specification but was obtained in electronic forms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 652;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              format from USPTO at segdata.uspto.gov/sequence.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 36; DB 8; 1
Pred. No. 1.6e+02;
2; Mismatches 2;
Claim 1; SEQ ID NO 15165; 122pp; English
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Matches 7; Conservative
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Gaps

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2; Indels

1 ASIAAARVLDY 11

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ADS26132 standard; protein; 652 AA.

RESULT 5 ADS26132

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Gaps

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Best Local Similarity 70.0 Matches 7; Conservative

2 SIAAARVLDY 11

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21

|:| ||||:| SVAQARVLEY

12

Sequence 652 AA;

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provide for expression of a polynucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant having an improved property. The plant is a crop plant comprising the recombinant DNA construct and growing the transformed plant where the avoing an improved property comprises transforming a plant with the recombinant DNA construct and growing the transformed plant, where the polynucleotide or polypeptide is useful for improving plant properties.

The recombinant DNA construct is useful for producing plant properties. The recombinant DNA construct is useful for producing plant properties. The recombinant DNA construct is useful for producing plant toperance, to lerance to herbicides, extreme osmocic conditions, pathogens or pests, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of content, improved yield by modification of carbohydrate, introgen or phosphorus use and/or uptake, by modification of photosynthesis or by providing improved plant growth and development under at least one stress condition, improved lignin production or improved galactomannan condition, improved lignin production or improved galactomannan condition, improved lignin production or improved galactomannan completed for mpart of the printed specification but was obtained in electronic correct form part of the printed specification but was obtained in electronic correct form part of the printed specification but was obtained in electronic correct correct or production. The sequence data for this patent did not correct form part of the printed specification but was obtained in electronic correct corrections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.
                                                                                                                                                                                                                                                                                                     Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; cold tolerance; nest tolerance; pathogen tolerance; pathogen tolerance; pathogen tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomanna; bacterial polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a recombinant DNA construct comprising a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Goldman BS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 14688; 122pp; English.
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                                                                                                                    ADS25655 standard; protein; 652 AA
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                                                                                                                                                                                                                                                           Bacterial polypeptide #14688.
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                                                                                                                                                                                                             (first entry)
255 AATAAARAIDY 265
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HINKLE G J.
SLATER S C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2004-061375/06.
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                                                                                                                                                               ADS25655;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria.
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(SLAT/)
(CHEN/)
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                                                                                              ADS2565E
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The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polymucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a cransformed plant having an improved property. The plant is a crop plant cauch as mainze or soybean. The method of producing a transformed plant cauch as mainze or soybean. The method of producing a plant with the cacombinant DNA construct and growing the transformed plant, where the polymucleotide or polypeptide is useful for improving plant properties. The recombinant DNA construct is useful for improving plants with construct is useful for improving plants with construct is useful for improving plants with construct is useful for improved plant properties. Contens of increased resistance to plant disease, better growth rate by modification content improved yield by modified seed oil or protein yield and/or content, improved yield by modification of photosynthesis or by prospertice of phosphorus use and/or uptake, by modification of photosynthesis or by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.
                                                                                                                                                                                                                                                                                                                                                                           cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis; pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomannan; bacterial polypeptide.
                                                                                                                                                                                                                                                                                                                                                            Recombinant DNA construct; transformed plant; improved plant property;
                                                    Gaps
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                      1.6e+02;
                Length 652;
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              Score 36; DB 8;
Pred. No. 1.6e+02
2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chen X,
                                                                                                                                                                                                                 ADS25373 standard; protein; 655 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Slater SC,
                                                                                                                                                                                                                                                                                                                          Bacterial polypeptide #14406.
                72.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-FEB-2003; 2003US-00369493
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                                                      Conservative
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255 AATAAARAIDY 265
                                                                                      1 ASIAAARVLDY 11
Ouery Match
Best Local Similarity
7; Conserv?
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SLATER S C.
CHEN X.
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                                                                                                                                                                                                                                                     ADS25373;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (SLAT/)
(CHEN/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HINK/)
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providing improved plant growth and development under at least one stress condition, improved lignin production or improved galactomannan production. This sequence represents a bacterial polypeptide used in the scope of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at segdata.uspto.gov/sequence.html.
                                                                                                                                                                                                      Sequence 655 AA;
   88888888888
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Gaps ; 0 72.0%; Score 36; DB 8; Length 655; 63.6%; Pred. No. 1.6e+02; ive 2; Mismatches 2; Indels Ouery Match
Best Local Similarity 63.00

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1 ASIAAARVLDY 11

|: |||| :|| 255 AATAAARAIDY 265

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ADS22602 standard; protein; 656 AA

(first entry) 02-DEC-2004

Bacterial polypeptide #11635.

cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis; pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomannan; bacterial polypeptide. Recombinant DNA construct; transformed plant; improved plant property;

Bacteria

US2003233675-A1

18-DEC-2003.

20-FEB-2003; 2003US-00369493.

21-FEB-2002; 2002US-0360039P.

(CAOY/)

CAO Y.
HINKLE G J.
SLATER S C.
CHEN X. (HINK/)

(CHEN/) CHEN X. (GOLD/) GOLDMAN B S.

Chen X, Hinkle GJ, Slater SC, Cao Y,

Goldman BS;

WPI; 2004-061375/06.

New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.

Claim 1; SEQ ID NO 11635; 122pp; English.

The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant having an improved property. The plant is a crop plant such as maize or soybean. The method of producing a transformed plant having an improved property comprises transforming a plant with the recombinant DNA construct and growing the transformed plant, where the polynucleotide or polypeptide is useful for improving plant properties. The recombinant DNA construct is useful for producing plants with

improved plant properties, e.g. improved cold, heat or drought tolerance, tolerance to harbicides, extreme osmotic conditions, pathogens or pests, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of homologous recombination, modified seed oil or protein yield and/or content, improved yield by modification of carbohydrate, introgen or prosphorus use and/or uptake, by modification of photosynthesis or by providing improved plant growth and development under at least one stress condition, improved lignin production or improved galactomannan production. This sequence represents a bacterial polypeptide used in the scope of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at segdata.uspto.gov/sequence.html

8888888888888888888

Sequence 656 AA;

Gaps ö Length 656; 72.0%; Score 36; DB 8; Length 656 63.6%; Pred. No. 1.7e+02; ive 2; Mismatches 2; Indels Query Match
Best Local Similarity 63.0

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1 ASIAAARVLDY 11

255 AATAAARAIDY 265

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RESULT

ABB48560 standard; protein; 708 AA

ABB48560;

05-FEB-2002 (first entry)

Listeria monocytogenes protein #1264

Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation; vitamin B12; bacterial infection; disease.

Listeria monocytogenes.

WO200177335-A2

18-OCT-2001

11-APR-2001; 2001WO-FR001118.

11-APR-2000; 2000FR-00004629.

(INSP) INST PASTEUR

C, Frangeul L, Couve E, Rusniok C, Fsihi H, Dehoux P; O, Chetouani F, Nedjari H, Glaser P, Kunst F, Cossart P; Goebel W, Kreft J, Kuhn M, Ng E, Vazquez-Boland JA; Berral G, Garrido-Garcia P, Tierrez-Martinez A, Amend A; Y T, Domann E, Hain T, Berche P, Charbit A, Durant L; J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N; De Pablos B, Wehland J, Kaerst U, Entian K, Hauf J; Chakraborty T, Domann E, Perez-Diaz J, Baquero F, Maduenio E, De Pablos B, Rose M, Voss H; Daniels J, Goebel W Dominguez-Bernal G, Jussurget O, Buchrieser

WPI; 2002-010914/01.

Genomic sequence for Listeria monocytogenes, useful e.g. for treatment and prevention of Listeria and related bacterial infections, and related polypeptides.

Claim 6; SEQ ID NO 1265; 192pp; French.

The present invention relates to the genome sequence of Listeria monocytogenes EGD-e (see ABA03041). The genome sequence and fragments of it are useful for selecting probes and primers for detecting genes in L. monocytogenes and related organisms, and for studying genetic polymorphisms and other genomes. The present sequence is a protein encoded by the genome sequence of the present invention. Proteins

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18-JUN-1999;
18-JUN-1999;
18-JUN-1999;
18-JUN-1999;
18-JUN-1999;
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27-JUL-1999;
27-JUL-1999;
                   20-MAY-1999;
21-MAY-1999;
25-MAY-1999;
25-MAY-1999;
27-MAY-1999;
01-JUN-1999;
                                                                                  03-JUN-1999;
04-JUN-1999;
07-JUN-1999;
08-JUN-1999;
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16-JUN-1999;
17-JUN-1999;
18-JUN-1999;
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18-JUN-1999;
18-JUN-1999;
21-JUN-1999;
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30-JUN-1999;
01-JUL-1999;
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18-JUN-1
18-JUN-1
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expressed from the genome sequence are useful for raising specific antibodies, identification of L. monocytogenes and related organisms, and for biosynthesis and biodegradation, especially biosynthesis of Vitamin B12. The genome sequence and proteins encoded by it are also useful for selecting compounds that regulate gene expression and cell replication and modulate L. monocytogenes-related diseases. In addition, the genome sequence and proteins encoded by it are useful in pharmaceutical and vaccines compositions for the treatment or prevention of infections by L. monocytogenes and related organisms. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from NIPO at five.yipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                               Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence; corn.
                                                                                                                                                            Gaps
                                                                                                                                                           ;
0
                                                                                                                                       Score 35; DB 5; Length 708;
Pred. No. 2.9e+02;
                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                  Zea mays protein fragment SEQ ID NO: 19948.
                                                                                                                                                          2; Mismatches
                                                                                                                                                                                                                                            AAG18510 standard; protein; 157 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                       990S-0125788P.
990S-0126264P.
990S-0126765P.
990S-0128234P.
990S-0128714P.
990S-0130077P.
990S-0130449P.
990S-0130449P.
990S-0130449P.
990S-0130448P.
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990S-0132486P
990S-0132487P
990S-0134256P
990S-0134218P
990S-0134219P
990S-01342119P
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99US-0123180P.
99US-0123548P.
                                                                                                                                         70.0%;
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                                                                                                                                                                                                                                                                               17-OCT-2000 (first entry)
                                                                                                                                       Query Match
Best Local Similarity 75.0
Matches 6; Conservative
                                                                                                                                                                                              697 AAARIIDY 704
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05-MAR-1999;
09-MAR-1999;
23-MAR-1999;
25-MAR-1999;
20-MAR-1999;
06-APR-1999;
06-APR-1999;
16-APR-1999;
16-APR-1999;
116-APR-1999;
21-APR-1999;
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04-MAY-1999;
05-MAY-1999;
06-MAY-1999;
06-MAY-1999;
07-MAY-1999;
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14-MAY-1999;
14-MAY-1999;
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23-APR-1999;
28-APR-1999;
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9905-0134768P 9905-0134941P 9905-0135353P 9905-0135353P 9905-0136392P 9905-0136392P 9905-0136392P 9905-0137522P 9905-0137522P 9905-0137522P 9905-0137522P 9905-0137522P 9905-0139453P 9905-0140354P 9905-0140354P 9905-0140354P 9905-0140353P 9905-0140353P 9905-0144332P 9905-0144333P 9905-0144333P 9905-0144333P 9905-0144333P 9905-0144333P 9905-0144333P 9905-0144332P 9905-0144332P 9905-0144332P 9905-0144332P 9905-0144332P 9905-0144332P 9905-0144332P 9905-0144332P 9905-0144332P

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990S-0145145P. 990S-0145218P. 990S-014524P. 990S-0145276P. 990S-0145913P.

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990S-0145919P

990S-0145951P

990S-0146388P

990S-0147038P

990S-0147038P

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990S-0147038P

990S-0147192P

990S-014913P

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990S-015139P

990S-015108P

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990S-015139P

990S-01609PP

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 27 - TUL - 1999, 28 - VUL - 1999, 28 - VUL - 1999, 28 - VUL - 1999, 22 - VUL - 1999, 22 - VUL - 1999, 23 - VUL - 1999, 24 - VUL - 1999, 25 - V
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05-0CT-1999;
06-0CT-1999;
12-0CT-1999;
13-0CT-1999;
13-0CT-1999;
14-0CT-1999;
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14-0CT-1999;
14-0CT-1999;
12-0CT-1999;
21-0CT-1999;
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24-SEP-1999;
28-SEP-1999;
29-SEP-1999;
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25-FEB-2000; 2000EP-00301439

-FEB-1999; -MAR-1999;

EP1033405-A2

06-SEP-2000

99US-0121825P.
99US-0123180P.
99US-012548P.
99US-0126284P.
99US-0126284P.
99US-0126284P.
99US-0128234P.
99US-0128434P.
99US-0130449P.
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-MAY-1999; -MAY-1999; -MAY-1999;

03-MAR-1999; 23-MAR-1999; 25-MAR-1999; 26-MAR-1999; 01-APR-1999; 06-APR-1999; 16-APR-1999; 19-APR-1999; 23-APR-1999; 23-APR-1999; 23-APR-1999; 30-APR-1999;

99US-0135629P. 99US-0136021P. 99US-0136392P.

24-MAY-1999; 25-MAY-1999; 27-MAY-1999;

14-MAY-1999; 14-MAY-1999; 14-MAY-1999; 18-MAY-1999;

11-MAY-1999 14-MAY-1999 07-MAY-1999

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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence; corn.
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                                                                                                                                                                                                            DB .
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                                                                                                                                                                                                               68.0%; Score 34; DB
ilarity 100.0%; Pred. No. 90;
Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAG18509 standard; protein; 159 AA
99US-0161359P.
99US-016136DP.
99US-016132DP.
99US-016192DP.
99US-0161933P.
99US-0161933P.
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                                                                                                                                                                                                                                                                                                                       5 AARVLDY 11
                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 7; Conserv
  26-OCT-1999;
26-OCT-1999;
26-OCT-1999;
28-OCT-1999;
28-OCT-1999;
29-OCT-1999;
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AAGI 8509

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AAGI 17-C

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AAGI 17-C

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9US - 0147302P 9US - 0147192P 9US - 0147260P 9US - 0147416P 9US - 0147416P 9US - 0147493P 9US - 0148171P 9US - 0148319P 9US - 0148319P 9US - 0148341P 9US - 0148341P	9019-0149426P 9019-0149723P 9018-0149723P 9018-0149929P 9018-0149930P 9018-0151068P 9018-0151068P 9018-0151068P 9018-0151068P 9018-0151080P 9018-0151080P 9018-0151080P 9018-0151080P 9018-0151080P 9018-0151080P 9018-0151080P 9018-0151080P 9018-0151080P 9018-0151080P 9018-0151080P 9018-0151080P 9018-0151080P 9018-0151080P 9018-0151080P 9018-0151080P 9018-0151080P	99US-01580229. 99US-0158232P. 99US-015823P. 99US-015929P. 99US-015929P. 99US-015929P. 99US-015923P. 99US-015933P. 99US-015933P. 99US-015933P. 99US-015963P. 99US-016074P. 99US-016074P. 99US-016074P. 99US-016074P. 99US-016074P. 99US-016074P. 99US-01608P. 99US-01608P. 99US-01608P. 99US-016192P. 99US-016140P. 99US-016140P. 99US-016140P. 99US-016140P. 99US-016140P. 99US-016140P. 99US-016140P. 99US-016192P.
04-AUG-1999 05-AUG-1999 06-AUG-1999 06-AUG-1999 06-AUG-1999 09-AUG-1999 09-AUG-1999 09-AUG-1999 11-AUG-1999 11-AUG-1999 11-AUG-1999 11-AUG-1999 11-AUG-1999	20-AUG-1999 3 20-AUG-1999	PR 07-0CT-1999; PR 13-0CT-1999; PR 13-0CT-1999; PR 13-0CT-1999; PR 13-0CT-1999; PR 14-0CT-1999; PR 14-0CT-1999; PR 21-0CT-1999; PR 21-0CT-1999; PR 21-0CT-1999; PR 21-0CT-1999; PR 21-0CT-1999; PR 21-0CT-1999; PR 22-0CT-1999; PR 22-0CT-1999; PR 22-0CT-1999; PR 22-0CT-1999; PR 25-0CT-1999; PR 26-0CT-1999;

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New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.
                                                                                Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; drought tolerance; heat bethicide; osmosis; pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomannan; bacterial polypeptide.
                                                                                                                                                                                                                                                                                                                                                                           Cao Y, Hinkle GJ, Slater SC,
                                                                                                                                                                                                                                                      20-FEB-2003; 2003US-00369493
                                                                                                                                                                                                                                                                              21-FEB-2002; 2002US-0360039P.
                                                         Bacterial polypeptide #17091
                                    02-DEC-2004 (first entry)
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HINKLE G J.
SLATER S C.
                                                                                                                                                                                                                                                                                                                                                   GOLDMAN B S
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                                                                                                                                                                                                      US2003233675-A1.
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             ADS28058;
                                                                                                                                                                                 Bacteria.
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                                                                                                                                                                                                                                                                                                                             (SLAT/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAX36754-Y37949 are encoded by open reading frames (ORFS) of the genome of Chlamydia trachomatis (see AAZ01425). The polypeptides can be used as vaccines against Chlamydia trachomatis. Antisense and ribozyme sequences can also be used to control growth of the microorganism. Chlamydia trachomatis is responsible for a large number of diseases, e.g. eye pleases such as conventional trachoma, nonendemic trachoma, paratrachoma, and inclusion conjunctivitis; genital diseases such as nongonococcal uretritis, epidymitis, cervicitis, salpingitis, epidymitis perhappatitis, bartholinitis; pneumopachy in breast feeding infants; and venereal lymphogranulomatosis. The polypeptides of the invention may be of use in treating these diseases
                                                                                                                                                                                                                                                    paratrachoma, inclusion conjunctivitis, genital disease, perihepatitis, nongonococcal uretritis, epidymitis, cervicitis, salpingitis, bartholinitis, pneumopathy, venereal lymphogranulomatosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                    Gaps
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            Length 159;
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Pred. No. 1e+02;
                                    0; Indels
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                                                                                                                                                                                                                   Amino acid sequence of a Chlamydia trachomatis protein.
            OB 3;
91;
                                    Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genome sequence of Chlamydia trachomatis.
            Score 34;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 1426; 1755pp; English.
                                                                                                                                           AAY37904 standard; protein; 180 AA
  68.0%; Suration of Prec
                                                                                                                                                                                                                                                                                                                                                                                                   97FR-00015041.
97FR-00016034.
98US-0107077P.
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77.8%;
                                                                                                                                                                                            (first entry)
Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity 77.8
7; Conservative
                                                                                                                                                                                                                                                                                                      Chlamydia trachomatis.
                                                                                 119 AARVLDY 125
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                                                         5 AARVLDY 11
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                                                                                                                                                                                           07-OCT-1999
                                                                                                                                                                                                                                                                                                                             W09928475-A2
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04-NOV-1998;
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Best Local S
                                                                                                                                                                    AAY37904;
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Goldman BS;

Chen X,

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promoter functional in a plant cell, where the promoter is positioned to promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant having an improved property comprises transformed plant with the recombinant DNA construct and growing the transformed plant with the recombinant DNA construct and growing the transformed plant, where the polynucleotide or polypeptide is useful for improving plant with the improved plant properties, e.g. improved cold, heat or drought tolerance, tolerance to herbicides, extreme comments, pathogens or peste, increased resistance to plant disease, better growth rate by modification to the content, improved yield by modification of carbohydrate, nitrogen or phosphorus use and/or uptake, by modification of phosphorus use to be property and and/or property where the plant plant growth register or property increased rate of the property or phosphorus use and/or uptake, by modification of phosphorus in the plant property at the plant plant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              providing improved plant growth and development under at least one stress condition, improved lignin production or improved galactomannan production. This sequence represents a bacterial polypeptide used in the scope of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gape
                                                                                                                                          invention relates to a recombinant DNA construct comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
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Pred. No. 1.4e+02;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  format from USPTO at segdata.uspto.gov/seguence.html
Claim 1; SEQ ID NO 17091; 122pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68.0%;
80.0%;
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Best Local Similarity 80.v.
89.v.
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ADS28058 standard; protein; 231 AA.

RESULT 13 ADS28058

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990S-0140899P.
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  18 - JUN - 1999

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06-AUG-1999;
06-AUG-1999;
09-AUG-1999;
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13-AUG-1999;
16-AUG-1999;
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05-AUG-1999
    Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                          Arabidopsis thaliana protein fragment SEQ ID NO: 22440.
                                                                             AAG20306 standard; protein; 237 AA
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990S-0123180P

990S-0125188P

990S-012664P

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990S-0128234P

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99US-0139452P.
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99US-0139492P.
99US-0139454P.
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                                                                                                                                 (first entry)
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100 ATIAAARKLD 109
                                                                                                                                                                                                                                      Arabidopsis thaliana
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25 MAY - 1999
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14-MAY-1999;
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18-MAY-1999;
20-MAY-1999;
21-MAY-1999;
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05-MAR-1999,
23-MAR-1999,
25-MAR-1999,
10-APR-1999,
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                                                                                                                                 17-OCT-2000
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                                                                                                       AAG20306;
                                                     RESULT 14
                                                                  AAG20306
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                 Arabidopsis thaliana protein fragment SEQ ID NO: 65899.
                                                                                                                                                                                                                                                 99US-0121825P.
99US-0123180P.
99US-012548P.
99US-012564P.
99US-0126748P.
99US-0126748P.
99US-012674P.
99US-012874P.
99US-012874P.
99US-0130891P.
99US-0132448P.
99US-0132448P.
99US-013248P.
99US-013422P.
99US-013424P.
99US-0134454P.
99US-0139453P.
                                                                                                                                                                                                                          25-FEB-2000; 2000EP-00301439
                                        18-OCT-2000 (first entry)
                                                                                                                                             Arabidopsis thaliana
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10-70N-1999;
14-70N-1999;
16-70N-1999;
16-70N-1999;
17-70N-1999;
18-70N-1999;
18-70N-1999;
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06-MAY-1999;
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27-MAY-1999;
28-MAY-1999;
01-JUN-1999;
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25-MAR-1999
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07-JUN-1999
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                 AAG51887;
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Pred. No. 1.4e+02;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity 100.0%; Por 7; Conservative 0;
990S-0149175P.
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990S-0149929P.
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                        20-AUG-1999;
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23-AUG-1999;
25-AUG-1999;
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24-SEP-1999;
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04-OCT-1999;
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06-OCT-1999;
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08-OCT-1999;
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Best Local S:
Matches 7
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99US-0139459P. 99US-0139460P. 99US-0139461P.

18-JUN-1999; 18-JUN-1999; 18-JUN-1999;

AAG51887 standard; protein; 237 AA.

RESULT 15 AAG51887 ID AAG518

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RR 18-JUN-1999; 99US-0139462P.
RR 18-JUN-1999; 99US-0139763P.
RR 18-JUN-1999; 99US-0139763P.
RR 21-JUN-1999; 99US-0139763P.
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RR
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PR 22-SEP-1999 9904-015104P

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PR 27-CEP-1999 9904-0160P

PR 27-CEP-1999 9904-0160P
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Search completed: October 14, 2005, 16:12:40 Job time : 85.5625 secs

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Gaps

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GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
               Copyright
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- protein search, using sw model OM protein October 14, 2005, 16:02:59; Search time 15.2969 Seconds (without alignments) 69.190 Million cell updates/sec Run on:

US-10-614-959-12 50 Title: Perfect score:

1 ASIAAARVLDY 11 Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	3-methylcrotonyl-C	3-methylcrotonyl-C	hypothetical prote	probable membrane	teichoic acid bios	carboxymethylenebu	thermitase (EC 3.4	methyltransferase			probable transcrip	DNA polymerase III	probable DNA polym	conserved hypothet	hypothetical prote		hypothetical prote		cobyrinic acid a,c	glycine dehydrogen	glutamyl-tRNA synt	membrane protein E	hypothetical prote		methionyl aminopep	histidinol-phospha	hypothetical prote	carbohydrate kinas	N-carbamoyl-beta-a
SUMMARIES	QI .	AF2984	A98299	S43071	S56849	AE1210	D87715	SUMYTV	140371	T38883	B71468	AF1059	AF2831	B97609	F89878	G69213	T45400	C70858	C84904	A75619	H70463	G82104	S45053	T27970	T06165	E85437	G69502	D64640	7	AG2869
	DB	~	•						•	•		•			•		•	•	•				7		•		•	~	•	~
	Query Match Length	663	709	143	692	969	231	279	579	649	926	162	202	202	220	264	358	367	397	441	482	509	614	1027	1232	305	342	363	365	409
d	Query Match	72.0	72.0	70.0	70.0	70.0	68.0	68.0	68.0	68.0	68.0	96.0	0.99	0.99	0.99	0.99	0.99	99	0.99	0.99	0.99	0.99	0.99	0.99	0.99	64.0	64.0	64.0	64.0	64.0
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## ALIGNMENTS

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3-methylcrotonyl-CoA carboxylase alpha subunit [imported] - Agrobacterium tumefaciens (s

C;Species: Agrobacterium tumefaciens
C;Date: 11.-Jan-2002 #sequence_revision 11.-Jan-2002 #text_change 09-Jul-2004
C;Date: 11.-Jan-2002 #sequence_revision 11.-Jan-2002 #text_change 09-Jul-2004
C;Accession: AF2984
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, Lerage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
Science 284, 2117-2233, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,

ster, E.W. A,Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens CS8. A,Reference number: AB2577; MUID:21608550; PMID:11743193

A;Accession: AF2984
A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-663 «KUR»
A;Cross-references: UNIPROT:Q8UA95; GB:AE008689; PIDN:AAL44292.1; PID:g17741880; GSPDB:G
A;Experimental source: strain C58 (Dupont)

C;Genetics:

A;Gene: mccA

A;Map position: linear chromosome C;Superfamily: propionyl-CoA carboxylase alpha chain; biotin carboxylase homology; lipoy

Gaps ö Query Match 72.0%; Score 36; DB 2; Length 663; Best Local Similarity 63.6%; Pred. No. 27; Matches 7; Conservative 2; Mismatches 2; Indels

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1 ASIAAARVLDY 11 ठ

258 AATAAARAIDY 268 셤

### RESULT 2

"methylcrotonyl-CoA carboxylase alpha chain (AF310338) [imported] - Agrobacterium tumef C; Species: Agrobacterium tumefaciens C; Species: Agrobacterium tumefaciens C; Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004 C; Accession A98299 R; Goddner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2332-2338, 2001 A; Liu, P.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; A; Litle: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum A; Reference number: A97359; MUID:21608551; PMID:11743194

A;Status: preliminary A;Molecule type: DNA A;Residues: 1-709 <KUR>

A;Cross-references: UNIPROT:Q8UA95; GB:AE007870; PIDN:AAK89915.1; PID:g15159866; GSPDB:G

A; Gene: AGR L 2704

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70.0%; Score 35; DB 2; Length 692; 70.0%; Pred. No. 45; 1; Indels rative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                     A;MOlecule type: DNA
A;Residues: 1-692 <SOR>
A;Cross-references: EMBL:X88851; NID:g895892; PID:g895898
                                            A;kesidues: 135-692 <VAM>
A;Cross-references: EMBL:Z34288; NID:g498992; PID:g498993
R;Sor, F.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Keywords: transmembrane protein
F;585-655/Domain: dnaJ amino-terminal homology <DNJ>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: SGD:S0003609; MIPS:YJL073w
A;Map position: 10L
C;Keywords: transmembrane protein
                                                                                                                                                                                                                      submitted to the EMBL Data Library, June 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 70.0
Matches 7; Conservative
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hes 6; Conservative
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245 SLAAAIILDY 254
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685 AAARIIDY 692
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A;Status: preliminary
                                                                                                                                                                                                                                                                                                      A; Accession: S57736
A; Accession: S47117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Gene: SGD: JEM1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Gene: 1mo1085
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A; Accession: S56847
A; Accession: S56847
A; Residues: 135-692 < POH->
A; Residues: 135-692 < POH->
A; Cross-references: BMBL:Z49348; MIPS:YJL073w
A; Cross-references: BMBL:Z49348; MIPS:YJL073w
A; Cross-references: BMBL:Z49348; MIPS:YJL073w
A; Cross-references: BMBL:Z49348; MID:95282514; PMID:7762302
A; Title: Sequence of a 17.1 kb DNA fragment from chromosome X of Saccharomyces cerevisia A; Reference number: S50798; MID:95282514; PMID:7762302
A; Reference number: S50798
A; Reterence number: S50798
A; Reterence number: S50798
A; Rolecule type: DNA
A; Reterences: EMBL:Z4288; NID:9498992; PIDN:CAA84049.1; PID:9498993
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1994
B; Vandenbol, M: Durand, P: Dion, C:; Portetelle, D:; Hilger, F.
Submitted to the EMBL Data Library, June 1994
A; Reference number: Sequence analysis of a 17.1 kb DNA fragment from chromosome X of Saccharc
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N.Alternate names: hypothetical protein HRC558; hypothetical protein J1083

C.Species: Saccharomyces cerevisiae

C.Species: Saccharomyces cerevisiae

C.Species: Saccharomyces cerevisiae

C.Species: Saccharomyces cerevisiae

C.Species: Saccharomyces revision 08-Sep-1995 #text_change 09-Jul-2004

C.Accession: S56849; S56847; S50798; S47117; S57736

S.Roseidue to the Protein Sequence Database, September 1995

A.Reference number: S56848

A.Recession: S56848

A.Residues: 1-692 <ROS

A.Residues: 1-692 <ROS

A.Residues: 1-692 <ROS

A.Residues: 1-692 <ROS

A.Residues: Sequence Batabase, September 1995

R.Yandenbol, M.; Durand, P.; Portetelle, D.; Hilger, F.

Submitted to the Protein Sequence Database, September 1995
A;Map position: linear chromosome
C;Superfamily: propionyl-CoA carboxylase alpha chain; biotin carboxylase homology; lipoy
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                                                                                                                        Score 36; DB 2; Length 709;
Pred. No. 29;
2; Mismatches 2; Indels
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                                                                                                                            Query Match 72.0%;
Best Local Similarity 63.6%;
Matches 7; Conservative
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Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                           304 AATAAARAIDY 314
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7 ASLAAARVL 15
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teichoic acid biosynthesis protein B homolog lmo1085 [imported] - Listeria monocytogenes
                                 C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Accession. ZE1210
C;Accession. ZE1210
C;Accession. ZE1210
C;Accession. ZE1210
B;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker'
C;Accession. Zernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
A;Authors: Schlueter, T.; Sinoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
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C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20.Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession: D8715
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Haft, D.H.; Kolon
B.; Gaub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzbary, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Residues: 1-696 <GLA>
A;Cross-references: UNIPROT:Q8Y833; GB:NC_003210; PIDN:CAC99163.1; PID:g16410487; GSPDB
A;Experimental source: strain EGD-e
C;Genetics:
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Rimurphy, L.; Harris, D.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
submitted to the EMBL Data Library, February 1996
A; Reference number: 221807
A; Accession: T19883
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-649 <MUR>
A; Cross-references: UNIPROT: Q10211; EMBL: Z69380; PIDN: CAA93342.1; GSPDB:GN00066; SPDB:SP
A; Experimental source: strain 972h-; cosmid c443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              probable insulinase family/proteinase III - Chlamydia trachomatis (serotype D, strain UW C; Species: Chlamydia trachomatis
C; Species: Chlamydia trachomatis
C; Species: Chlamydia trachomatis
C; Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 09-Jul-2004
C; Accession: B71468
R; Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell, Science 282, 784-759, 1998
A; Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trac: A; Reference number: A71570; MUID:99000809; PMID:9784136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: UNIPROT:084812; GB:AE001353; GB:AE001273; NID:g3329271; PIDN:AAC6840 A;Experimental source: serotype D, strain UW-3/Cx
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A;Note: this species has also been called Salmonella typhi
C;Date: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
R;Parkhill, J; Dougan, G; James, K.D.; Thomson, N.R.; Pickard, D; Wain, J.; Churcher, th, T; Connerton, P; Cronin, A; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S; Moule, S; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quall, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;tile: Complete genome sequence of a multiple drug resistant Salmonella enterica serov A;Reference number: AB0502; MUID:21534947; PMID:11677608
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                                                            lypothetical protein SPAC4H3.03c - flssion yeast (Schizosaccharomyces pombe)
                                                                                C;Species: Schizosacharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T38883
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C;Superfamily: Schizosaccharomyces pombe hypothetical protein SPAC4H3.03c
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631 AAIAAAHILD 640
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916 IAAARSMDY 924
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nes 7; Conserv
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A;Status: preliminary
A;Molecule type: DNA
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FEBS Lett. 183, 195-200, 1985
A;Title: Complete primary structure of thermitase from Thermoactinomyces vulgaris and iq
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C;Genetics:
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methyltransferase - Bacillus stearothermophilus (fragment)
C;Species Bacillus stearothermophilus
C;Species Bacillus stearothermophilus
C;Species Bacillus stearothermophilus
C;Accession: 140371
K;Rina, M.; Markaki, M.; Bouriotis, V.
Gene 150, 71-73, 1994
A;Title: Sequence of the cloned bseCIM gene: M.BseCI reveals high homology to M.BanIII.
A;Reference number: 140371; MUID:95047552; PMID:7959066
A;Reference climinary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-579 <-RES.
                                                     A;Cross-references: UNIPROT:Q9A213; GB:AE005673; NID:g13425534; PIDN:AAK25720.1; GSPDB:C_igenetics:
C_igenetics:
A;Gene: CC3758
C;Superfamily: carboxymethylenebutenolidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: protein
A; Residues: 1-279 < MRI.>
A; Residues: 1-279 < MRI.>
A; Cross-references: UNIPROT: P04072
C; Comment: This protein is enzymatically similar to a proteinase from Streptomyces sp. C; Superfamily: subtilisin; subtilisin homology
C; Supervords: hydrolase; serine proteinase
F; 29-239/Domain: subtilisin homology < SBT.>
F; 38,71,225/Active site: Asp, His, Ser #status predicted
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C;Species: Thermoactinomyces vulgaris
C;Date: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 09-Jul-2004
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26 AEVIAKRILDY 36
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A; Accession: A00973
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nes 8; Conserva
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Best Local Similarity
Matches 6; Conserva
A; Molecule type: DNA
A; Residues: 1-231 <STO>
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A,Cross-references: UNIPROT.Q99V10; GB:BA000018; PID:g13700889; PIDN:BAB42185.1; GSPDB:GASTerimental source: strain N315; Genetical source: strain N315; A; Genetical source: strain N315; C; Superfamily: conserved hypothetical protein MG323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein MTH852 - Methanobacterium thermoautotrophicum (strain Delta H) (jaceies: Methanobacterium thermoautotrophicum c;bate: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004 C;Accession: G69213 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004 C;Accession: G69213 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004 C;Accession: G69213 #sequence_revision 05-Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Rismith, D.R.; Dadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N. ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N. J. Harlie: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct A;Reference number: A69000; MUID:98037514; PMID:9371463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A)Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Rosidues: 1.264 eMTH-
A;Cross-references: UNIPROT:026940; GB:AE000862; GB:AE000666; NID:g2621943; PIDN:AAB8535;
A;Experimental source: strain Delta H
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54.5%;
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Best Local Similarity 54.5
Matches 6; Conservative
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94 ASIAAVKLINY 104
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131 NVASASVLDY 140
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                                                                 156 ASIAAARAL 164
      1 ASIAAARVL 9
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A, Molecule type: DNA
A, Residues: 1-220 < KUR>
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A.Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum A.Reference number: A97359; MUID:21608551; PMID:11743194
A.Reference number: A97359; MUID:21608551; PMID:11743194
A.Residues: preliminary
A.Molecule type: DNA
A.Residues: 1-202 <KUR>
A.Residues: 1-202 <KUR>
A.Cross-references: UNIPROT:QBUDP4; GB:AE007869; PIDN:AAK87827.1; PID:g15157207; GSPDB:GC;Genetics:
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A,Status: preliminary
A,Redecule type: DNA
A,Residues: 1-202 «KUR»
A,Residues: 1-202 «KUR»
A,Cross-references: UNIPROT:Q8UDP4; GB:AE008688; PIDN:AAL43068.1; PID:g17740536; GSPDB:G
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R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell; Kaperco, P.; Zhang, S. Science 294, 2317-2323, 2001

A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
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A, Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A, Reference number: AB2577; MUID: 21608550; PMID: 11743193
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A; Molecule type: DNA
A; Residues: 1-162 <PAR>
A; Cross-references: GB: AL513382; PIDN: CAD06923.1; PID:g16505571; GSPDB:GN00176
C; Genetics:
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Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
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Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
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                                                                                                                                    October 14, 2005, 15:51:44 ; Search time 73.2188 Seconds (without alignments) 76.932 Million cell updates/sec
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R. HISSP: P24182; 1DV1.
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Basaki T., Matsumcto T., Yamamoto K., Sakata K., Baba T., Katayose Y.,
Wu J., Niimura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H.,
Hosokawa S., Masukawa M., Arikawa K., Chiden Y., Hayashi M.,
Okamoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C.,
Hijishita S., Honda M., Ichikawa Y., Idonuma A., Iijima M., Ikeda M.,
Ikeno M., Itoh S., Itoh T., Itoh Y., Itoh Y., Iwabuchi A., Kamiya K.,
Karasawa W., Katagiri S., Kikuta A., Kobayashi T., Mukai Y.,
Machita K., Machara T., Mizuno H., Mizubayashi T., Mukai Y.,
Nagasaki H., Nakashima M., Nakamari Y., Nakamura M.,
Nagasaki H., Nakashima M., Ohta I., Ono N., Saji S., Sakai, K., Shibata M.,
Shimokawa T., Shomura A., Song J., Takazaki Y., Terasawa K., Tsuji K.,
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Name=P0022E10.15;
Oryza sativa (japonica cultivar-group).
Bukaryota; Viridiplantes; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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InterPro; IPR001882; Biotin Garb C.
InterPro; IPR000482; Biotin Lipoyl.
InterPro; IPR0005401; Cphg Byrin L D2.
InterPro; IPR00105401; Cphg Synth L D2.
InterPro; IPR011054; Hybrid motif.
InterPro; IPR011054; Rudmnt hyb motif.
Ffam; PF00344; Biotin carb C; I.
Ffam; PF00349; Ebsase L chain; I.
Pfam; PF002186; CPSase L chain; I.
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GO; GO:0009374; F:bictin binding; IEA.
GO; GO:0016874; F:ligase activity; IEA.
GO; GO:0018152; P:metabolism; IEA.
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SEQUENCE 694 AA: 75656
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268 AAVAAAKAIDY 278
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Best Local Similarity
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Q8S2E4
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Waki K., Yamagata H., Yamane H., Yoshiki S., Yoshihara R., Yukawa K., Zhong H., Iwama H., Endo T., Ito H., Hahn J.H., Kim H.I., Eun M.Y., Yano M., Jiang J., Gojobori T.; "The genome sequence and structure of rice chromosome 1."; Nature 420:312-316(2002).
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
NCBI_TaxID=39947;
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Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
--- SINTLARITY: Belongs to the ABC transporter family.
EMBL; AJ535055; CAD59577.1; -.
HSSP; P08716; 1MT0.
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EMBL; AP003229; BAB89499.1; -.
HSSP; P08716; 1MT0.
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1-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
MDR-like ABC transporter.
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Pred. No. 1.9e+02;
2; Mismatches 1;
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InterPro; IPR003593; AAA ATPase.
InterPro; IPR01527; ABC membrane I. InterPro; IPR01140; ABC membrane I.
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Length 402; 0, Indels

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PubMed=1537794;
Holden M.T.G., Titball R.W., Peacock S.J., Cerdeno-Tarraga A.M.,
Atkins T., Crossman L.C., Pitt T., Churcher C., Mungall K.,
Bentley S.D., Sebathia M., Thomson N.R., Bason N., Beacham I.R.,
Brooks K., Brown K.A., Brown N.F., Challis G.L., Cherevach I.,
Chillingworth T., Cronin A., Crosset B., Davis P., Cherevach I.,
Reltwell T., Fraser A., Hance Z., Hauser H., Holroyd S., Jagels K.,
Reth K.E., Maddison M., Moule S., Price C., Quail M.A.,
Rabbinowitsch E., Rutherford K., Sanders M., Simmonds M.,
Songsivial S., Stewens K., Tunapa S., Vesarachaves M.,
Mitchead S., Yeats C., Barrell B.G., Oyston P.C.F., Parkhill J.;
"Genomic plasticity of the causative agent of melloidosis,
Burkholderia pseudomallei.";
Burkholderia pseudomallei.";
Broc. Nall. Acad. Sci. U.S.A. 101:14240-14245(2004).
REBL; BX5/1966; CAH38304.1; -.
SEQUENCE 402 AA, 41596 MW; 6FCA16BE0F4B18EA CRC64;
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Nester E.W.,
The genome of the natural genetic engineer Agrobacterium tumefaciens
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01-070-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
3-methylorotonyl-CoA carboxylase alpha subunit.
Name-mccA, OrderedLocusNames-Atu3479;
Name-mcCA, OrderedLocusNames-Atu3479;
Baprobacterium tumefaciens (Brrain CS8 / ATCC 33970).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
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GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0016874; F:Ligase activity; IEA.
GO; GO:0008152; P:metabolism; IEA.
Féam; PF002185; Biotin carb C; 1.
Pfam; PF002185; Biotin—lipoyl; 1.
PROSITE; PS00188; BIOTIN; 1.
PROSITE; PS00188; BIOTIN; 1.
PROSITE; PS00186; CPSASE 1; UNKNOWN 1.
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EMBL; ARG09278; AL44292.1; -.
PIR; A98299; A98299.
PIR; AF2984; AF2984.
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Best Local Similarity 70...
Tr Conservative
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SEQUENCE 663 AA; 71187
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Q8UA95,
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                SORETTARARARARARAS
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Nierman W.C., DeShazer D., Kim H.S., Tettelin H., Nelson K.E.,
Peldblyum T., Ulrich R.L., Renning C.M., Brinkac L.M., Daugherty S.C.,
Davidson T.D., Deboy R.T., Dimitrov G., Dodson R.J., Durkin A.S.,
Gwinn M.L., Haft D.H., Khouri H., Kolonay J.F., Madupu R.,
Mohammoud Y., Nelson W.C., Radune D., Romero C.M., Sarria S.,
Selengut J., Shambin C., Sullivan S.A., White O., Yu Y., Zafar N.,
Zhou L., Fraser C.M.;
"Structural flexibility in the Burkholderia mallei genome.";
"Structural flexibility in the Burkholderia mallei genome.";
EMBL, CP000011; AJU46877.1; -.
SEQUENCE 402 AA, 41596 MW, 6FCA16BE0F4B18EA CRC64;
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
Putative transporter protein.
ORFNames=BPSS0842;
Burkholderia pseudomallei K96243.
Burkholderia, Proteobacteria; Betaproteobacteria; Burkholderiales;
NCBL TaxID=272560;
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Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Burkholderiaceae; Burkholderia.
NCBI_TaxID=243160;
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Pred. No. 2e+02;
2; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                        1234 AA; 134571 MW; C5F9E9D75D28AC93 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Major facilitator superfamily protein.
ORFNames=BMAA0712;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    402 AA
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InterPro; IPR003439; ABC transporter.
Pfam; PF00664; ABC membrane; 2.
Pr00005; ABC tran; 2.
Pr000m; PD000006; ABC transporter; 2.
SMART; SM0382; AAA; 2.
PROSITE; PS50929; ABC TMIF; 2.
PROSITE; PS50921; ABC TRANSPORTER 1; 2.
PROSITE; PS50931; ABC TRANSPORTER 2; 2.
ATP-binding.
SEQUENCE 1234 AA; 134571 WW; CSF9E9D75
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                                                                                                                                                                                                                                                                                                                                                                  74.0%;
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Best Local Similarity 70.0.
The 7; Conservative
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Matches 7; Conservative
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106 ATVAAARLLD 115
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Query Match

Q63M18 Q63M18;

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RESULT 6
063M18
1D 063M 063M
AC 063M 063M
DT 25-00
DT 25-

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Hypothetical protein OJ1172F09.9. Name=OJ1172F09.9;
                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                        NCBI_TaxID=39947;
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Q69X93
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MEDLINE=2160B551; PubMed=11743194; DOI=10.1126/science.1066803;

Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,

Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,

Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,

Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,

Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.,

"Genome sequence of the plant pathogen and biotechnology agent

Agrobacterium tumefaciens C58.";

Science 294:233-2336(2001).

EMBL, AB008334; AAR89915.1; -.

HSSP: P02905; 1BDO.
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OrderedLocusNames=AGR L 2704;

OrderedLocusNames=AGR L 2704;

Bacbacterium tumefaciens (strain C58 / ATCC 33970).

Bacteria; Protoboacteria; Alphaproteobacteria; Rhizobiales;

Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
  Score 36; DB 2; Length 663;
Pred. No. 1.7e+02;
2; Mismatches 2; Indels
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Last annotation update)
                                                                                                                                                                                                                                                                                         05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                709 AA.
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GO; GO: 1005524; F: ATP binding; IEA.
GO; GO: 1006874; F: Biotin binding; IEA.
GO; GO: 1006874; F: Biotin binding; IEA.
GO; GO: 1006872; P: Rilgase activity; IEA.
GO; GO: 1006812; P: Rilgase activity; IEA.
InterPro; IPR005482; Biotin ES.
InterPro; IPR005481; CPase L. N.
InterPro; IPR005481; CPase L. N.
InterPro; IPR011054; Rudmat hyb motif.
Ffam; PF02785; Biotin carb C; I.
Pfam; PF02785; Biotin carb C; I.
Pfam; PF02785; Biotin lipoyl; I.
Pfam; PF0289; CPSase L. chain; I.
PROSITE; PS00188; BIOTIN; I.
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PROSITE; PS00867; CPSASE 2; UNKNOWN 1
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    72.0%;
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Query Match 72.0
Best Local Similarity 63.6
Matches 7; Conservative
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Matches 7; Conservative
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258 AATAAARAIDY 268
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                                                                                            1 ASIAAARVLDY 11
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Q8H034
ID Q8H0:
AC Q8H0:
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STRAIN=DSME 1740:

MEDLINE=2882897; PubMed=14500908; DOI=10.1073/pnas.1932838100;

Baar C., Eppinger M., Raddatz G., Simon J., Lanz C., Klimmek O.,

Nandakumar R., Gross R., Rosinus A., Keller H., Jagtap P., Linke B.,

Meyer F., Lederer H., Schuster S.C.;

Meyer F., Lederer H., Schuster S.C.;

"Complete genome sequence and analysis of Wolinella succinogenes.";

Proc. Natl. Acad. Sci. U.S.A. 100:11690-11695(2003).

EMBL; BX571658; CAE09628.1; -.

GO; GO:0019861; C:flagellum; IRA.

InterPro; IPR009940; Prenyl_trans.

InterPro; IPR009941; TPR-like.
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Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Wolinella.
NCBI_TaxID=844;
Oryza sativa (japonica cultivar-group).
Sukaryota, Vizidiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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Hypothetical protein.
SEQUENCE 723 AA; 78613 MW; 3FD842215E6EDIFD CRC64;
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PROSITE; PS50293; TPR REGION; 1.
COMplete protecome; Flagellum.
SEQUENCE 778 AA; 89775 MW; 382P992CE949C27E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-WAR-2004 (TrEMBLrel. 26, Created)
01-WAR-2004 (TrEMBLrel. 26, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
FLAGELLAR FUNCTIONAL PROTEIN.
Name-PFLA; OrderedLocusNames=WS0490;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           72.0%; Score 36; DB 2; I
80.0%; Pred. No. 1.9e+02;
iive 1; Mismatches 1;
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Pred. No. 2e+02;
2; Mismatches
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63.6%;
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Best Local Similarity 63.6
Matches 7; Conservative
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616 ASLAAARVTD 625
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Gaps

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STRAIN=LSv54 / DSM 12343;
PubMed=15305914;
Rabus R., Ruepp A., Frickey T., Rattei T., Fartmann B., Stark M.,
Bauer M., Zibat A., Lombardot T., Becker I., Amann J., Gellner K.,
Teeling H., Leuschner W.D., Gloeckner F.-O., Lupas A.N., Amann R.,
Klenk H.-P.,
"The genome of Desulfotalea psychrophila, a sulfate-reducing bacterium
from permanently cold Arctic sediments.";
EMBL; CR522870; CAG35482.1; -.
"A transforming fragment within the direct repeat region of human herpesvirus type 6 that transactivates {\rm HIV-1."}_i, Oncogene 9:1167-1175(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Desulfotalea psychrophila.
Bacteria, Proteobacteria, Deltaproteobacteria, Desulfobacterales,
Desulfobulbaceae, Desulfotalea.
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Bacteria; Actinobacteria; Actinobacteriae; Streptomyces.
Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI_TaxID=1902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70.0%; Score 35; DB 2; Length 184; 80.0%; Pred. No. 81;
                                                                                                                                                                              Length 143;
                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                  Thompson J.T.;
Submitted (JUN-1993) to the EMBL/GenBank/DDBJ databases.
EMBL, 7313675; CRAS2028.1; -.
PIR; 543071, 843071.
SEQUENCE 143 AA; 13317 MW; EDF78898C3D31734 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                184 AA; 20792 MW; 8D9DCB5EDFAA60AF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Putative zinc.binding oxidoreductase.
ORFNames=SCF51.18;
                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                             Score 35; DB 2;
Pred. No. 63;
                                                                                                                                                                                                                                                                                                                                                       184 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        329 AA
                                                                                                                                                                                                            1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                    25-OCT-2004 (TrEMBLrel. 28, Created)
                                                                                                                                                                             70.0%;
                                                                                                                                                                                                                                                                                                                                                                                                25-OCT-2004 (TrEMBLrel. 28, 25-OCT-2004 (TrEMBLrel. 28, Hypothetical protein,
                                                                                                                                                              Query Match
Best Local Similarity 88.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                  OrderedLocusNames=DP0753;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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7 ASLAAARVL 15
                                                                                                                                                                                                                                         1 ASIAAARVL 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Complete proteome. SEQUENCE 184 AA;
                                                       [2]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=84980;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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Q6AQ91;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                          Oryza sativa (japonica cultivar-group).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Epermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
BEDLINE-24181269; PubMed=8134119;
Thompson J., Choudhury S., Kashanchi F., Doniger J., Berneman Z., Frenkel N., Rosenthal L.J.;
                                                                                                                                                                                                                                                                                                                   GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
InterPro; IPR011009; Kinase_like.
InterPro; IPR011009; Kinase_like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATP-binding; Kinase; Receptor; Serine/threonine-protein kinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                       SEQUENCE FROM N.A.
Sasaki I., Matsumoto I., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 6, PAC
                                                                                                                                                                                                                                                                      Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
-- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
EMBL; AP003622; BAD32908.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             72.0%; Score 36; DB 2; Length 1072; 80.0%; Pred. No. 2.7e+02; ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1072 AA; 114368 MW; E15B809971B15F78 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Humān herpesvirus 6.
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Betaherpesvirinae; Roseolovirus.
NCBI_TaxID=10368;
                                   25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Putative receptor-like protein kinase 2.
Name=P0633E08.13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Herpesvirus Type 6 DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS, PROGOUS, LEURICHRPT.

PRODOM, PROBOSO1, PROC. Kinase; 1.

SMART; SMO0269; LRR_TYP; 11.

SMART; SMO0219; TYKC; 1.

SMART; SMO0219; TYKC; 1.

PROSITE; PS0011; PROTEIN KINASE DAP; UNKNOWN_1.

PROSITE; PS0011; PROTEIN KINASE DAP; UNKNOWN_1.
         PRT; 1072 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         143 AA
                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001611; IRR.
InterPro; IPR007090; IRR plant.
InterPro; IPR0070391; IRR Lyp.
InterPro; IPR000719; Prot kinase.
InterPro; IPR008270; Ser thr pkinase.
InterPro; IPR008271; Ser thr pkin AS.
InterPro; IPR001245; Tyr pkinase.
Fam; PP00560; IRR 1; 22.
Pfam; PP00569; Pkinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match
Best Local Similarity 80.0
Best Aconservative
        PRELIMINARY;
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116 ASLAALRVLD 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                 GO; GO:0004024; F:alcohol dehydrogenase activity, zinc-dependent; IEA. GO; GO:0008270; F:zinc ion binding; IEA. InterPro; IPR002085; Adh zn family. InterPro; IPR011032; GroES_like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
MEDLINE=21996410; PubMed=12000953; DOI=10.1038/417141a; Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L., Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H., Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M., Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S., Huang C.-H., Kieser T., Larke L., Murphy L.D., Oliver K., O'Neil S., Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K., Warren T., Wietzorrek A., Woodward J.R., Barrell B.G., Parkhill J., Hopwood D.A.,
                                                                                                                                                                                                                                                                                      "Complete genome sequence of the model actinomycete Streptomyces coelicolor A3(2).";
Mature 417.141-147(2002).
EMBL; A193105; CAB59716.1; -.
HSSP; Q8L3C8; 11YZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FBB-1995 (Rel. 31, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 44, Last annotation update)
Hypochetical 80.4 kDa protein in SMC3-MRPL8 intergenic region.
OrderedLocusNames=VJL073W; ORFNames=J1083, HRC558;
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi, Ascomycota; Saccharomycetina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         70.0%; Score 35; DB 2; Length 329; 70.0%; Pred. No. 1.4e+02; ive 1; Mismatches 2; Indels
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Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Entian K.D.;
to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   329 AA; 34155 MW; 5DCAD4FB174FD042 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       692 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00107; ADH_zinc_N; 1
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189 SLGAAHVLDY 198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rose M., Koetter P.,
Submitted (SEP-1995)
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P40358;
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YJH3_YEAST
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Matches
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EMBL; X88851; CAA61312.1; -.

EMBL; X34288; CAA84049.1; -.

EMBL; X356849; S56849.

R PIR; S56849; S56849.

R RSP; POB622; 1BQZ.

Germonline; 141687; -.

GO; GO:0003609; JEMI.

GO; GO:0003767; F:co-chaperone activity; IGI.

GO; GO:0000742; P:karyogamy during conjugation with cellular . . .; IGI.

GO; GO:0006571; P:protein folding; IGI.

R GO; GO:0006457; P:protein folding; IGI.

R GO; GO:000672; P:protein folding; IGI.

SMART; SM0071; DnaJ; 1.

SMART; SM0071; DnaJ; 1.

R ROSITE; PS50076; DNAJ_1; PALSE_NEG.

R Hypothetical protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           692 AA; 80381 MW; 9F612DD16B66981B CRC64;
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Matches 7; Conservative
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SLAAAIILDY 254
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JS-09-383-667-12
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Sequence 19, Appl
Sequence 6, Appli
Sequence 10, Appli
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Sequence 622, App
Sequence 3417, Ap
Sequence 12051, A
Sequence 508, App
Sequence 3193, Ap
Sequence 17003, A
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31470, A
10906, A
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                                                                                                                                      October 14, 2005, 16:00:04; Search time 21.6562 Seconds (without alignments) 37.917 Million cell updates/sec
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Sequence 3
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/pcTTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/pcTTUS_COMB.pep:*
                      GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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US-09-348-667-19

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US-09-363-68-2

US-09-253-854-6

US-09-253-854-6

US-09-135-658-4

US-09-135-658-4

US-09-135-658-4

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US-09-135-658-4

US-09-136-18164

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Maximum Match 100%
Listing first 45 summaries
                                                                                                     OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length
                                       Copyright
                                                                                                                                                                                                                                 Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                    Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Database
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38, Appl
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38, Appl
38, Appl
38, Appl
55, Appl
55, Appl
45191, A
225, Appl
225, Appl
2274, A
2211, A
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                                Sequence Seq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 12, Application US/09383667
; Sequence 12, Application US/09383667
; Patent No. 6624295
; GENERAL INFORMATION:
; APPLICANT: Adams, Camelia W. APPLICANT: Beron, Dan L. APPLICANT: Eaton, Dan L. APPLICANT: Hass, Philip B. APPLICANT: Hass, Philip B. APPLICANT: Widdle, J. Kevin , APPLICANT: Suggett, Shelley TITLE OF INVENTION: Human Anti-Factor IX/IXA Antibodies TILE REFERENCE: P1661R2
; CURRENT APPLICANTON NUMBER: US 60/098,233
; EARLIER FILING DATE: 1999-08-26
; EARLIER PPLICATION NUMBER: US 60/122,767
; EARLIER APPLICATION NUMBER: US 60/122,767
; SEQ ID NO 12
; SEQ ID NO 12
; SEQ ID NO 12
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APPLICANT: Devaux, Brigitte
APPLICANT: Baton, Dan L.
APPLICANT: Judice, J. Kevin
APPLICANT: Judice, J. Kevin
APPLICANT: Xirchhofer, Daniel
APPLICANT: Suggett, Shelley
TITLE OF INVENTION: Human Anti-Factor IX/IXa Antibodies
FILB REFERENCE: P1661R2
                          US-09-295-028-38

US-09-028-55

US-09-106-582-55

US-09-1159-469-38

US-09-159-469-38

US-09-693-542-38

US-09-693-542-38

US-09-693-542-55

US-09-693-542-55

US-09-693-542-55

US-09-252-991A-2371

US-09-252-991A-2371

US-09-252-991A-2371

US-09-252-991A-28830

US-09-252-991A-28830

US-09-252-991A-28830

US-09-252-991A-2088

US-09-252-991A-2088

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US-09-60-902A-11
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100.0%; Score 50; DB 4; I
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 11; Conservative 0; Mismatches 0;
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; ORGANISM: Homo sapiens
US-09-383-667-12
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GENERAL INCORMATION:

APPLICANT: van de Ven, Willem Jan Marie
APPLICANT: van de Noweland, Anna Maria Wilhelmina
APPLICANT: van den Ouweland, Anna Maria Wilhelmina
APPLICANT: van den Ouweland, Anna Maria
APPLICANT: Robroek, Antonius Johannes Lambertus Petrus
APPLICANT: Robroek, Antonius Johannes Maria
APPLICANT: Koning, Piet Nico Maria
TITLE OF INVENTION: Pharmaceutical Composition Having An
TITLE OF INVENTION: Endoproteolytically Processing (Precursor)
TITLE OF INVENTION: Proteins And For The (Micro) Biological
TITLE OF INVENTION: Production Of Proteins
TITLE OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                           Endoproteolytically Processing (Precursor)
Proteins And For The (Micro)Biological
Production Of Proteins
         Endoproteolytic Activity; A Process for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 68.0%; Score 34; DB 2; Length 278; Best Local Similarity 80.0%; Pred. No. 25; Mstches 8; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: END COMPACTION
COMPUTER: END PC COMPACTION
COMPACTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PETENTIN Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/865,203
FILING DATE: 29-MAY-1997
CLASSIFFCATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Tran, J6ssica H.
REFERRNCE/DOCKET NUMBER: 294-41 DIV
TELECHOME: (516) 822-3550
TELEPHOME: (516) 822-3552
TITLE OF INVENTION: Endoproteolytical
TITLE OF INVENTION: Endoproteolytical
TITLE OF INVENTION: Proteins And For
TITLE OF INVENTION: Production Of Proteins Production Of Proteins OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOFPMANN & BARON, LLP
STREET: 350 Jericho Turnpike
CITY: Jericho
STATE: New York
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 6, Application US/07849420
; Patent No. 5989856
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STREET: 30 Rockefeller Plaza
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 278 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , MOLECULE TYPE: protein US-08-865-203-6
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US-07-849-420-6
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Pred. No. 30;
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Sequence 6, Application US/08865203
Settent No. 5935815
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: van de Ven, Willem Jan Marie
APPLICANT: van den Ouweland, Anna Maria Wilhelmina
APPLICANT: van Duijnhoven, Johannes Lambertus Petrus
APPLICANT: Robrock, Antonius Johannes Maria
APPLICANT: Robrock, Antonius Johannes Maria
APPLICANT: Piet Nico Maria
TITLE OF INVENTION: Pharmaceutical Composition Having An
                                                                                                                                                                                                                                                                                                                  Score 46; DB 4; Length 11;
Pred. No. 0.0013;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/09342648
Patent No. 6248584
GENERAL INFORMATION:
APPLICANT: Cahoon, Rebecca E.
APPLICANT: Cahoon, Rebecca E.
APPLICANT: Rafalski, Antoni
APPLICANT: Rafalski, Antoni
APPLICANT: Rafalski, Antoni
FILE OF INVENTION: Transcription Coactivators
FILE OF ILLING DATE: 1999-166-29
CURRENT APPLICATION NUMBER: US/09/342,648
CURRENT PILING DATE: 1999-66-29
EARLIER APPLICATION NUMBER: 60/092,659
EARLIER FILING DATE: July 13, 1998
NUMBER OF SEQ ID NOS: 10
                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
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                           CURRENT FILING DATE: 1999-08-26
EARLIER APPLICATION NUMBER: US 60/098,233
EARLIER FILING DATE: 1998-08-28
EARLIER APPLICATION NUMBER: US 60/122,767
EARLIER FILING DATE: 1999-03-03
NUMBER OF SEQ ID NOS: 32
LENGTH: 11
         CURRENT APPLICATION NUMBER: US/09/383,667
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                                                                                                                                                                                                                                                                                                                     92.0%;
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SEQ ID NO 2
LENGTH: 755
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Best Local Similarity 90.5
Matches 10; Conservative
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                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity
Matches 8; Conserv
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ORGANISM: Zea mays
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LOCATION: (179)
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LOCATION: (185)
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US-09-342-648-2
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US-08-865-203-6
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Query Match
Best Local Similarity 80.0
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Best Local Similarity 80.0
Matches 8; Conservative
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APPLICANT: van den Ouweland, Anna Maria Wilhelmina;
APPLICANT: van den Ouweland, Anna Maria Wilhelmina;
APPLICANT: van Duijhnoven, Johannes Lambertues Petrus;
APPLICANT: Robroek, Antonius Johannes Maria; and
APPLICANT: Koning, Piet Nico Maria
TITLE OF INVENTION: Pharmaceutical Composition Having An
TITLE OF INVENTION: Endoproteolytically Process for
TITLE OF INVENTION: Endoproteolytically Processing (Precursor)
TITLE OF INVENTION: Proteins And For The (Micro)Biological
TITLE OF INVENTION: Production Of Proteins
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Pred. No. 25;
0; Mismatches 2; Indels
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 19920624
CLASSIFICATION: 435
ATTONNEY/AGENT INFORMATION:
NAME: Moran, Thomas F.
REGISTRATION NUMBER: 16,579
REFERENCE/DOCKET NUMBER: 2805/41413
TELECHONE: (212) 977-9550
TELECAMINICATION INFORMATION:
TELECAMINICATION INC. 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 278 amino acids
TURES: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: HOFFMANN & BARON, LLP
STREET: 350 Jericho Turnpike
CITY: Jericho
STATE: New York
COUNTRY: U.S.A.
ZIP: 11753
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.24
CURRENT APPLICATION NUMBER: US/09/253,854
FILING DATE: UNABRIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-253-854-6
; Sequence 6, Application US/09253854
Setent No. 6132717
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Tran, J0881Ca H.
REGISTRATION NUMBER: 40,846
REFERENCE/DOCKET NUMBER: 294--
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 822-3550
TELEFAX: (516) 822-3582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-849-420-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ||| | ||||
96 ASILAVRVLD 105
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68.0%; Score 34; DB 4; Length 279; 80.0%; Pred. No. 25; 2; Indels ive 0; Mismatches 2; Indels
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      Sequence 9, Application US/09196281A

Patent No. 6605438

GENERAL INFORMATION:
APPLICANT: Banden. Peter K.
APPLICANT: Banditz, Peter
APPLICANT: Banditz, Peter
APPLICANT: Mikkelsen, Frank
TILE OF INVENTION: Protease Variants And Compositions
FILE REFERENCE: 5435.200-US
CURRENT APPLICATION NUMBER: US/09/196,281A
CURRENT APPLICATION NUMBER: 1332/97
EARLIER FILING DATE: 1999-11-21
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 12
5472855-6

; PATENT (CARTER, PAUL J.; WELLS, JAMES A. TITLE OF INVENTION: SUBSTRATE ASSISTED CATALYSIS NUMBER OF SEQUENCES: 31

; CURRENT APPLICATION DATA: BAPPLICATION NUMBER: 105/08/287,964

PRIOR APPLICATION NUMBER: 90,902

FILING DATE: 12-3EP-1994

; PRIOR APPLICATION NUMBER: 823,039

FILING DATE: 12-JUL-1993

APPLICATION NUMBER: 35,652

FILING DATE: 04-APR-1987

APPLICATION NUMBER: 334,081

FILING DATE: 01-DEC-1987

APPLICATION NUMBER: 127,134

FILING DATE: 01-DEC-1986

APPLICATION NUMBER: 846,627

FILING DATE: 01-APR-1986

APPLICATION NUMBER: 614,612

FILING DATE: 30-APR-1986

APPLICATION NUMBER: 614,612

FILING DATE: 30-APR-1986

APPLICATION NUMBER: 614,615

FILING DATE: 29-MAY-1984

APPLICATION NUMBER: 614,615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 34; DB 6;
Pred. No. 25;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 29-MAY-1984
APPLICATION NUMBER: 614,491
FILING DATE: 29-MAY-1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68.0%;
80.0%;
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Best Local Similarity 80.0
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ASIAAARVLD 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                LENGTH: 279
TYPE: PRT
CRGANISM: Bacillus
US-09-196-281-9
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                                                            Score 34; DB 2; Length 279;
Pred. No. 25;
0; Mismatches 2; Indels
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Pred. No. 25;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 34; DB 4; Length 279;
Pred. No. 25;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                              US-09-512-251A-6

Sequence 6, Application US/09512251A

Sequence 6, Application US/09512251A

GENERAL NOORMATION:
APPLICANT: Hansen, Peter
APPLICANT: Bauditz, Peter
APPLICANT: Andersen, Kim
TITLE OF INVENTION: Protease Variants and Compositions
FILE REFERENCE: 5349-204-US
CURRENT APPLICANION NUMBER: US/09/512,251A

CURRENT FILING DATE: 2000-02-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 6, Application US/09515150A

Patent No. 6558938

GENERAL INFORMATION:
APPLICANT: Hanean, Peter
APPLICANT: Mikkelsen, Frank
APPLICANT: Andersen, Kim
TILLE OF INVENTION: Protease Variants and Compositions
FILE REFERENCE: 5348.204-US
CURRENT APPLICATION NUMBER: US/09/515,150A

CURRENT APPLICATION NUMBER: 2000-02-29
NUMBER OF SEQ ID NOS: 12

SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6
LENGTH: 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68.0%;
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80.0%;
                                                               Query Match
Best Local Similarity 80.0%;
Matches 8; Conservative
; ORGANISM: Bacillus subtilis
US-09-135-658-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 80.0
Matches 8; Conservative
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Best Local Similarity 80.0
Matches 8; Conservative
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ORGANISM: Bacillus
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LENGTH: 279
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US-05-710-279-622
US-05-710-279-622
Sequence 622, Application US/09710279
Fatent No. 6703492
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
CURRENT FILING DATE: 2000-11-09
FRIOR FILING DATE: 1999-11-09
FRIOR FILING DATE: 1999-11-09
FRIOR FILING DATE: 2000-11-09
FRIOR FILING DATE: 2000-11-09
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US-09-710-279-622
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                                                                                                                                                                                                                      Query Match 66.0%; Score 33; DB 4; Length 85; Best Local Similarity 70.0%; Pred. No. 9.8; Matches 7; Conservative 1; Mismatches 2; Indels
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Job time : 22.6562 secs
OTHER INFORMATION: Gap in alignment FEATURE:
                                                             NAME/KEY: MISC_FEATURE
1 LOCATION: (30)...(33)
2 OTHER INFORMATION: Gap in alignment
US-09-698-286A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 60.0
Matches 6; Conservative
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106 NVASASVLDY 115
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71 SIAAGKPLDY 80
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APPLICANT: University of Kentucky Research Foundation
TITLE OF INVENTION: Human REVI Gene and Protein As Diagnostic, Preventive, and Therap
FILE REPERBYCE: 050229-0247
CURRENT FILING DATE: 2000-10-30
PRIOR APPLICATION NUMBER: 60/162,140
PRIOR PLING DATE: 1999-10-29
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin version 3.1
SEQ ID NO 10
LENGTH: 85
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ORGANISM: C. elegans, A. thaliana, S. cerevisiae, S. pombe and H. sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68.0%; Score 34; DB 6; Length 279; 80.0%; Pred. No. 25; ive 0; Mismatches 2; Indels
                                                                             RESULT 13
5472855-6
i Patent No. 5472855
i Patent No. 5472855
i TITLE OF INVENTION: SUBSTRATE ASSISTED CATALYSIS
i NUMBER OF SEQUENCES: 31
i CURRENT APPLICATION DATA:
APPLICATION NUMBER: 105/08/287,964
i FILING DATE: 22-SEP-1994
i PRIOR APPLICATION DATA:
APPLICATION NUMBER: 90,902
i FILING DATE: 12-JUL-1993
APPLICATION NUMBER: 823,039
i FILING DATE: 04-APR-1987
APPLICATION NUMBER: 35,652
FILING DATE: 04-APR-1989
APPLICATION NUMBER: 35,652
FILING DATE: 01-DEC-1987
APPLICATION NUMBER: 127,134
FILING DATE: 01-DEC-1987
APPLICATION NUMBER: 846,627
FILING DATE: 01-APR-1986
APPLICATION NUMBER: 846,627
FILING DATE: 01-APR-1986
APPLICATION NUMBER: 614,612
FILING DATE: 29-MAY-1984
APPLICATION NUMBER: 614,615
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NAME/KEY: MISC_FEATURE
LOCATION: (17)..(22)
OTHER INFORMATION: Gap in alignment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 29-MAY-1984
APPLICATION NUMBER: 614,491
PILING DATE: 29-MAY-1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 80.0
Matches 8; Conservative
      96 ASILAVRVLD 105
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NAME/KEY: MISC FEATURE
LOCATION: (50)..(60)
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US-09-698-286A-10
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18892, A 17091, A 5, Appli 9, Appli

Title: Perfect score:

Sequence:

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Run on:

Scoring table:

Searched:

Minimum DB E Maximum DB E

Database

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Sequence 369042, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: APPLICANT: Acvalic, David K.
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(5322)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 369042
LENGTH: 183
                                                                     Sequence 17091, A Sequence 6, Applia Sequence 953435, A Sequence 45651, A Sequence 70274, A Sequence 122779, Sequence 122779, Sequence 6707, Applia Sequence 1707, Applia Sequence 1707, Applia Sequence 1807, Applia Sequen
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Pred. No. 7.9;
0; Mismatches 1; Indels
6 US-10-437-963-201347
6 US-10-767-701-3892
5 US-10-369-493-17091
4 US-10-369-493-17091
6 US-10-403-105-9
6 US-10-403-105-9
6 US-10-403-105-9
6 US-10-403-105-3
70-10-369-493-703-3
70-10-369-493-703-3
8 US-10-369-493-703-3
10-10-425-114-402-8
8 US-10-425-114-4080-8
9 US-10-282-1227-6-8
9 US-10-67-476-50
9 US-10-67-476-50
9 US-10-67-476-50
9 US-10-67-476-50
9 US-10-417-700A-49
9 US-10-417-700A-49
9 US-10-417-700A-49
9 US-10-412-115-189243
9 US-10-422-115-189243
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US-10-425-115-369042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: unsure
LOCATION: (1)..(183)
OTHER INFORMATION: unsure at all Xaa locations
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Best Local Similarity 90.0
Matches 9, Conservative
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642
642
671
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203
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331
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ORGANISM: Zea mays
FEATURE:
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JS-10-425-115-369042
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Sequence 4311, App
Sequence 45544, A
Sequence 208239,
Sequence 120758,
Sequence 120758,
Sequence 15165, A
Sequence 15165, A
Sequence 11635, A
Sequence 11635, A
Sequence 11635, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                            October 14, 2005, 16:20:10; Search time 78.2031 Seconds (without alignments) 58.615 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
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14: /cgn2_6/ptodata/2/pubpaa/USO0_NEW PUB.pep:*
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                           GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd
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US-10-389-566-831
US-10-425-114-45544
US-10-425-115-208229
US-10-425-115-208239
US-10-437-963-120758
US-10-369-493-14688
US-10-369-493-14406
US-10-369-493-14406
US-10-369-493-14406
US-10-369-493-1406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                1859788 segs, 416717961 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                    protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                          BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seg length: 0
seg length: 200000000
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Match
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Sequence 63141, A Sequence 53, Appl Sequence 53, Appl

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1 ASIAAARVLDY 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Zea mays
JS-10-425-115-208229
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CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 45544
                                        SUBJECT STATES OF STATES O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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COCATION: (103)...(104)
COTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-10-389-566-831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 37; DB 15; Length 408;
Pred. No. 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Clone ID: 700800359_FLI.pep
US-10-425-114-45544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-425-114-45544
; Sequence 45544, Application US/10425114
; Publication No. US20040034888A1
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ASIAAARVLDY 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          275 ASLAAARALD 284
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ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Zea mays
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58 ANIADTRVLDY 68

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APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Sovalic, David K.
APPLICANT: Stou, Yihua
APPLICANT: Caou, Yihua
APPLICANT: Cao, Yongwan
TITLE OF INVENTION: Plants
FILE OF INVENTION: Plants
FILE REPERENCE: 38-21 [3322] B
CURRENT FILING DATE: 2003-04-28
SEQ ID NO 208229
LENGTH: 573
LENGTH: 573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: La Royalicw:
APPLICANT: La Royalic, David K.
APPLICANT: Scotlic, David K.
APPLICANT: Shou, Yihua
APPLICANT: Shou, Yihua
APPLICANT: Cap. Yongwin
TITLE OF INVENTION: Nacleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REPERENCE: 38-21 [53122] B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
SEQ ID NOS: 369326
SEQ ID NO 208239
LENGTH: 694
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Pred. No. 1.3e+02;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 573;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                            ; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_121499C.l.pep
US-10-425-115-208229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , OTHER INFORMATION: Clone ID: MRT4577_121507C.1.pep
US-10-425-115-208239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 37; DB 16;
Pred. No. 1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-437-963-120758
; Sequence 120758, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Roosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
Sequence 208229, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-425-115-208239
; Sequence 208239, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
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Best Local Similarity 72.7.

Section 8; Conservative
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Best Local Similarity 72.7
Matches 8; Conservative
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Gaps

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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Gao, Yongwei

APPLICANT: Hinkle, Gregory J.

APPLICANT: Hinkle, Gregory J.

APPLICANT: Glodman, Barry S.

APPLICANT: Goldman, Barry S.

APPLICANT: Chen, Xianfeng

TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROPERTIES

TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

FILE REFERENCE: 38-10(52052)B

CURRENT APPLICATION NUMBER: US 60/360,039

PRIOR FILING DATE: 2003-02-28

PRIOR FILING DATE: 2002-02-21

NUMBER: OF SEQ ID NOS: 47374
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                                                                                                                                                                                                                                                                                                                                                                             Query Match 72.0%; Score 36; DB 15; Length 652; Best Local Similarity 63.6%; Pred. No. 1.9e+02; Matches 7; Conservative 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 36; DB 15; L Pred. No. 1.9e+02; 2; Mismatches 2;
FILE REFERENCE: 38-10 (52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 15165
LENGTH: 652
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Agrobacterium tumefaciens US-10-369-493-14406
                                                                                                                                                                                                                                                                                        ORGANISM: Agrobacterium tumefaciens US-10-369-493-15165
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Best Local Similarity 63...
7; Conservative
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255 AATAAARAIDY 265
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255 AATAAARAIDY 265
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US-10-369-493-11635
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Sequence 14680, Application US/10369493

Bedication No. US20030233675A1

GENERAL INFORMATION:
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Marry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROPERIUS
TITLE OF INVENTION: BLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28

PRIOR FILING DATE: 2002-02-21

NUMBER OF SEQ ID NOS: 47374

SEQ ID NO 14688

LENGTH: 652
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei, Wei
APPLICANT: Buckharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Barbazuk, Brad
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 120758
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Sequence 15165, Application US/10369493
Publication No. US20030233675A1
Sembral INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Cao, Xianten
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Pred. No. 2.3e+02;
2; Mismatches 1; Indels
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Pred. No. 1.9e+02;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Clone ID: PAT_MRT4530_2384C.1.pep
US-10-437-963-120758

i TYPE: PRT
i ORGANISM: Agrobacterium tumefaciens
US-10-369-493-14688

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Best Local Similarity 63.6
Matches 7; Conservative
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Matches 7; Conservative
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255 AATAAARAIDY 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           330 ASVAATRILD 339
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ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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Gaps

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APPLICANT: Li, Ping Till, Ping TILL OF INVENTION: Acid Molecules and Other Molecules Associated With TILL OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REPERIOR: 138-21 (53221) B CURRENT APPLICATION NUMBER: US/10/437,963 CURRENT FILING DATE: 2003-05-14 NUMBER OF SEQ ID NOS: 204966 SEQ ID NO 175236 LENGTH: 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 38892, Application US/10767701
| Sequence 38892, Application US/10767701
| Publication No. US20040172684A1
| Septence 38892, Application No. US20040172684A1
| GENERAL INFORMATION:
| APPLICANT: Kovalic, David K.
| APPLICANT: Cao, Yongwei
| TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
| TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
| FILE REPERENCE: 38-21(5335) B
| CURRENT APPLICATION NUMBER: US/10/767,701
| CURRENT PILING DATE: 2004-01-29
| NUMBER OF SEQ ID NOS: 63128
| SEQ ID NOS: 63128
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                                                                                        Length 45;
                                                                                                                               Indels
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OTHER INFORMATION: Clone ID: SORBI-28MAY03-C77436_1.pep
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US-10-437-963-175236
      ; OTHER INFORMATION: Clone ID: PAT_MRT4530_96731C.1.pep
US-10-437-963-201347
                                                                                   70.0%; Score 35; DB 16;
88.9%; Pred. No. 18;
artive 0; Mismatches 1
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OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                                                                                                                                                                                                                              Sequence 175236, Application US/10437963; Publication No. US20040123343A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Wu, Wei
APPLICANT: Bucharov, Andrey A.
                                                                                                                                    Conservative
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ORGANISM: Sorghum bicolor
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34 ASLAAARVSD 43
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ORGANISM: Oryza sativa
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16 SIATARVLD 24
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Matches 8; Conserv
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Matches 8; Conserv
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Sequence 189046, Application US/10437963

Publication No. US20040123343A1

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Cao, Yongwei

APPLICANT: Barbaruk, Brad

APPLICANT: Barbaruk, Brad

APPLICANT: Li, Ping

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE OF INVENTION: DAY 153221)B

CURRENT APPLICATION NUMBER: US/10/437,963

CURRENT PILING DATE: 2003-05-14

NUMBER OF SEQ ID NOS: 204966

SEQ ID NO 189048

LEGGTH: 1064
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; Sequence 201347, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Cao, Vinua
; APPLICANT: Cao, Yongwei
; APPLICANT: Buukharov, Andrey A.
; APPLICANT: Buukharov, Andrey A.
; APPLICANT: Buukharov, Andrey A.
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; TITLE OF INVENTION: Plants
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; LENGTH: 45
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80.0%; Pred. No. 3.2e+02;
iive 1; Mismatches 1; Indels
                                                                                                        Score 36; DB 15; Length 65
Pred. No. 1.9e+02;
2; Mismatches 2; Indels
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US-10-437-963-189048
; LENGTH: 656
; TYPE: PRT
; ORGANISM: Agrobacterium tumefaciens
US-10-369-493-11635
                                                                                                           72.0%;
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Best Local Similarity 80.v-
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Best Local Similarity 63.00
Reference 7; Conservative
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255 AATAAARAIDY 265
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116 ASLAALRVLD 125
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ORGANISM: Oryza sativa
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ORGANISM: Oryza sativa
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Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels
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114 AARVLDY 120
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US-10-767-701-38892
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US-10-369-493-17091
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Search completed: October 14, 2005, 17:00:43 Job time : 79.2031 secs

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Compugen Ltd.
 GenCore version (c) 1993 - 2005
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sw model - protein search, using OM protein

October 14, 2005, 15:51:19; Search time 99.9375 Seconds (without alignments) 50.310 Million cell updates/sec Run on:

US-10-614-959-13 66

SGSTSNIGNNYVS 13 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2105692 seqs, 386760381 residues

2105692 Total number of hits satisfying chosen parameters:

length: 0 length: 200000000 sed Minimum I Maximum I

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A_Geneseq_16Dec04:*
1: geneseq_1980s:*
2: geneseq_p1990s:*
3: geneseq_p2000s:* geneseqp1980s:* geneseqp1990s:* geneseqp2000s:* geneseqp2001s:* geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* geneseqp2004s:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

u	Anti-fact	Anti-adip	Human BLy	Single ch	Neurokini	Neurokini	Human BLy	Human CMO	Single ch			Neurokini		Single ch	TNF proli	Chemokine	Neurokini	Neurokini	Human BLy						
Description	Aay79071	Aau 02544	Aau02558	Aau02612	Aau02627	Aau02629	Aau02542	Aau02551	Abp45887	Adg96714	Adg34301	Adg34317	Abp45916	Aao31147	Adg96743	Adg34310	Adg34306	Adg34303	Abp45915	Adg96742	Adg98057	Ade83862	Adg34308	Adg34313	Abp45902
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ABP45906 ADG96733 ADG96729	ADE83872 ABP45671 ABP45432 ABP45923	ABP45917 ABP45696 ABP45888	ADG30413 ADG30455 ADG96715 ADG96498	ADG96259 ADG96750 ADG96523	ADE83874 ADG34304
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## ALIGNMENTS

Complementarity determining region 1, CDR1; antibody; Gla domain; factor IX/XIx; blood coagulation; deep venous thrombosis; light chain; arterial thrombosis; unstable angina; post myocardial infarction; coronary artery bypass graft; CABG; stroke; tumour growth; metastsasis; percutaneous transluminal coronary angioplasty; PTCA; inflammation; septic shock; hypotension; adult respiratory distress syndrome; ARDS; arterial fibrillation; disseminated intravascular coagulopathy; DIC. Anti-factor IX/IXa antibody L chain V domain CDR1 amino acid sequence. AAY79071 standard; peptide; 13 AA. 12-JUN-2000 (first entry) AAY79071; AAY 79071

LU AAY 79071

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WO200012562-A1. Homo sapiens. 09-MAR-2000. 99WO-US019453. 26-AUG-1999; 98US-0098233P. 99US-0122767P. 28-AUG-1998; 03-MAR-1999;

(GETH ) GENENTECH INC.

Devaux B, Eaton DL, Hass PE, Judice JK, Kirchhofer D; Adams CW, Suggett S;

WPI; 2000-256595/22.

Novel human anti-Factor IX/IXa antibodies against IX/IXa gamma-carboxyglutamic acid domains useful as anti-coagulant in thrombosis, stroke, and post myocardial infarction.

Claim 8; Fig 2; 84pp; English.

This sequence represents a complementarity determining region 1 (CDR1) of the light chain variable domain of a human anti-factor IX/IXa Gla domain antibody. Factor IXa is a vitamin K dependent plasma serine protease that participates in the blood coagulation pathways. To Gla domain of factor IXa and its zymogen factor IX contains important structural determinants for interaction with high affinity binding sites on vascular endothelial

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Panel of specific binding members of antibody molecules which bind to whole adipocytes is used in the treatment of obesity and obesity related
comprising the antibodies are used for prombotic or coagulopathic diseases or
      the treatment or prophylaxis of thrombotic or coagulopathic diseases of disorders in a mammal for which inhibiting a FIX/IXa mediated event is indicated, e.g. deep venous thrombosis, arterial thrombosis, unstable angina, post myocardial infarction, post surgical thrombosis, unstable angina, post myocardial infarction, post surgical thrombosis, coronary artery bypass graft (FABG), percutaneous transluminal coronary angiophasty (PTCA), stroke, tumour growth, invasion or metastasis, inflammation, septic shock, hypotension, adult respiratory distress syndrome (ARDS), arterial fibrillation and disseminated intravascular coagulopathy (DIC)
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Pred. No. 0.00029;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAU02544 standard; protein; 109 AA
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platelets. Compositions
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Matches 13; Conservative
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N-PSDB; AAS03444.
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sequences of anti-adipocyte monoclonal antibody heavy chain, light chain, and heavy chain complementarity determining regions (CDR) of the invention. The antibodies can be used in the treatment of boesity and obesity related diseases. The antibodies can be used to deliver drugs or pro-drugs directly to the far mass of an obese patient or the antibody can be used as a therapeutic itself, Antibodies binding specifically to adipocytes can be used to activate the immune system to destroy the cells by complement mediated lysis. The antibodies may be labeled with a detectable label such as radiolabel, fluorescent or chemical group and the cused in methods of diagnosis in human subjects e.g. to determine the presence or level of adipocytes in a cell or tissue sample. The antibodies can be used as an alternative means of treatment for obese patients other than undergoing surgery to remove excess fat. Antibodies for different types of fat deposits can also be produced e.g. intra-abdominal fat associated with heart disease
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for different types of fat deposits can also be produced e.g. intra-
abdominal fat associated with heart disease
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                                                                              Score 66; DB 4; Length 109;
Pred. No. 0.0026;
                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                   Antibody; adipocyte; heavy chain; light chain; obesity; heart disease; complementarity determining region; CDR.
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                                                                                 ; UB 0.0026;
                                                                                                           0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 128-129; 182pp; English.
                                                                                                                                                                                                                                                                   AAU02558 standard; protein; 110 AA.
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                                                                                100.0%;
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                                                                                                                                                                        SGSTSNIGNNYVS 35
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                                                                                                                  13; Conservative
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N-PSDB; AAS03458.
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Best Local Similarity
                                                                                                 Local Similarity
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                                                  Sequence 109 AA;
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                                                                                   Query Match
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Antibody; adipocyte; heavy chain; light chain; obesity; fat; heart disease; complementarity determining region; CDR.

Anti-adipocyte monoclonal antibody light chain, FAT 112.

(first entry)

29-AUG-2001

AAU02627 standard; protein; 110 AA.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and heavy chain complementarity determining regions (CDR) of the antibodies can be used in the treatment of obesity and obesity related diseases. The antibodies can be used to deliver drugs or pro-drugs directly to the fat mass of an obese patient or the antibody or pro-drugs directly to the fat mass of an obese patient or the antibody can be used as a therspeutic itself. Antibodies binding specifically to adjocytes can be used to activate the immune system to destroy the cells by complement mediated lysis. The antibodies may be labeled with a by complement mediated lysis. The antibodies may be labeled with a caterable label such as radiolabel, fluorescent or chemical group and used in methods of diagnosis in human subjects e.g. to determine the presence or level of adjocytes in a call or tissue sample. The antibodies can be used as an alternative means of treatment for obese patients other than undergoing surgery to remove excess fat. Antibodies con lifferent types of fat deposits can also be produced e.g. intra-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Panel of specific binding members of antibody molecules which bind to whole adipocytes is used in the treatment of obesity and obesity related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
                                                                                                                                                                                                                                                                                      fat;
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100.0%; Pred. No. 0.0026;
ive 0; Mismatches 0; Indele
                                                                                                                                                                                                                                                                                Antibody; adipocyte; heavy chain; light chain; obesity; heart disease; complementarity determining region; CDR.
                                                                                                                                                                                                                                                Anti-adipocyte monoclonal antibody light chain, FAT 99.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 abdominal fat associated with heart disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
                                                                                                                                        AAU02612 standard; protein; 110 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vaughan TJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 163; 182pp; English.
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                                                                                                                                                                                                               (first entry)
                                   23 SGSTSNIGNNYVS 35
                SGSTSNIGNNYVS 13
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                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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Best Local S
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                                                                                                                       AAU02612
ID AAU
                                                                                                      RESULT 4
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Panel of specific binding members of antibody molecules which bind to whole adipocytes is used in the treatment of obesity and obesity related

Claim 1; Page 172; 182pp; English.

diseases.

(CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.

11-OCT-2000; 2000WO-GB003900. 12-OCT-1999; 99US-0158812P

40200127279-A1 Homo sapiens.

19-APR-2001

Vaughan TJ;

Main SH,

Edwards BM,

WPI; 2001-282031/29. N-PSDB; AAS03527.

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ANU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
and heavy chain complementarity determining regions (CDR) of the
convention. The antibodies can be used in the treatment of obesity and
cobesity related diseases. The antibodies can be used to deliver drugs or
pro-drugs directly to the fat mass of an obese patient or the antibody
can be used as a therapeutic itself. Antibodies binding specifically to
adipocytes can be used to activate the immune system to destroy the cells
cathory complement mediated lysis. The antibodies may be labeled with a
detectable label such as radiolabel, fluorescent or chemical group and
used in methods of diagnosis in human subjects e.g. to determine the
presence of adipocyte antigen on the surface of an adipocyte to detect or
determine the presence or level of adipocytes in a cell or tissue sample.
The antibodies can be used as an alternative means of treatment for obese
patients other than undergoing surgery to remove excess fat. Antibodies
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abdominal fat associated with heart disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 66; DB 4; Length 110;
Pred. No. 0.0026;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 110 AA;
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Best Local Simi:
Matches 13; (
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ID AAU0
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SGSTSNIGNNYVS 35

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RESULT 5 AAU02627

1 SGSTSNIGNNYVS 13 13; Conservative

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sequences of anti-adipocyte monoclonal antibody heavy chain, light chain, and heavy chain complementarity determining regions (CDR) of the invention. The antibodies can be used in the treatment of obesity and obesity related diseases. The antibodies can be used to deliver drugs or pro-drugs directly to the far mass of an obese patient or the antibody can be used as a therapeutic itself. Antibodies binding specifically to adipocytes can be used as a therapeutic itself. Antibodies binding specifically to adipocytes can be used as a radiolabel, fluorescent or chemical group and by complement mediated lysis. The antibodies may be labeled with a detectable label such as radiolabel, fluorescent or chemical group and used in methods of diagnosis in human subjects e.g. to determine the presence or level of adipocytes in a cell or tissue sample. The antibodies can be used as an alternative means of treatment for obese patients other than undergoing surgery to remove excess fat. Antibodies for abdominal fat associated with heart disease
                                                                                                                                                                                                                                                                              Panel of specific binding members of antibody molecules which bind to whole adipocytes is used in the treatment of obesity and obesity related
                                                                                                                                                                                                                                                                                                                                                                                                                           AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
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                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 118-119; 182pp; English.
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                                                                                                                                                                Vaughan TJ;
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                          11-OCT-2000; 2000WO-GB003900.
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                                                                                                                                                                Edwards BM, Main SH,
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Best Local Similarity
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                                                                    12-0CT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid sequences of anti-adipocyte monoclonal antibody heavy chain, light chain, and heavy chain complementarity determining regions (CDR) of the invention. The antibodies can be used in the treatment of obesity and obesity related diseases. The antibodies can be used to deliver drugs or pro-drugs directly to the fat mass of an obese patient or the antibody can be used as a therapeutic itself. Antibodies binding specifically to adipocytes can be used to activate the immune system to destroy the cells by complement mediated lysis. The antibodies may be labeled with a detectable label such as radiolabel, fluorescent or chemical group and used in methods of diagnosis in human subjects e.g. to determine the presence or level of adipocytes in a cell or tissue sample. The antibodies can be used as an alternative means of treatment for obese contractive means of treatment for obese for different types of fat deposits can also be produced e.g. intra-abdominal fat associated with heart disease
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Antibody; adipocyte; heavy chain; light chain; obesity; fat; heart disease; complementarity determining region; CDR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 66; DB 4; Length 110; 100.0%; Pred. No. 0.0026; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Anti-adipocyte monoclonal antibody light chain, FAT 30.
                                                                                                                                                                                                                                                                                                           (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAU02542 standard; protein; 111 AA.
                                                                                                                                                                                                                                                                                                                                                         Vaughan TJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 173; 182pp; English.
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Best Local Similarity
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                                                                                                                       AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
and heavy chain complementarity determining regions (CDR) of the
invention. The antibodies can be used in the treatment of obesity and
charge directly to the fat mass of an obese patient or the antibody
can be used as a therapeutic itself. Antibodies binding specifically to
adipocytes can be used to activate the immune system to destroy the cells
by complement mediated lysis. The antibodies binding specifically to
adipocytes can be used to activate the immune system to destroy the cells
by complement mediated lysis. The antibodies may be labeled with a
detectable label such as radiolabel, fluorescent or chemical group and
used in methods of diagnosts in human subjects e.g. to determine the
presence of adipocyte antigen on the surface of an adipocyte to detect or
determine the presence or level of adipocytes in a cell or tissue sample.
The antibodies can be used as an alternative means of treatment for obese
for different types of fat deposits can also be produced e.g. intra-
abdominal fat associated with heart disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; manuosuppressive, immunostimulant; immunomodulatory; antirheumatic; antiAlDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency; systemic lupus erythematosus; rheumatoid arthritis; CVID; AlDS;
                                                 Panel of specific binding members of antibody molecules which bind to whole adipocytes is used in the treatment of obesity and obesity related
                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  common variable immunodeficiency; acquired immunodeficiency syndrome
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                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 66; DB 4; Length 111;
100.0%; Pred. No. 0.0027;
.ive 0; Mismatches 0; Indels
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CAMBRIDGE ANTIBODY TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human BLyS binding scFv SEQ ID 1898.
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                                                                                                  Claim 1; Page 124; 182pp; English
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2001US-0276248P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-MAR-2001; 2001US-0277379P.
25-MAY-2001; 2001US-0293499P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                       24 SGSTSNIGNNYVS 36
                                                                                                                                                                                                                                                                                                                                                                                                                                         1 SGSTSNIGNNYVS 13
                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
             2001-282031/29
                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
tes 13; Conserv
                                                                                                                                                                                                                                                                                                                                                               Sequence 111 AA;
                        N-PSDB; AAS0345
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16-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABP45887;
                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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                                                                          diseases
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This invention describes novel antibodies that immunospecifically bind to B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the tumour necrosis factor (TNF) super family and induces B cell colliseration and differentiation. The antibodies of the invention have cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antirheumatic and antiALDS activity of BLyS. The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in biological samples and may be used in this way to diagnose disease associated with aberrant expression of BLyS. They may also be ambinistered to treat diseases associated with aberrant BLyS expression and activity such as cancer, immune, and autoimmune disorders and diseases. e.g. systemic lupus erythematosus, rheumatoid architits, immunodeficiency (e.g. common variable immunodeficiency (cVID) and acquired immunodeficiency syndrome (AlDS)). ABB43290-ABB47228 represent
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                                                                                                                Antibodies against B Lymphocyte Stimulating polypeptides, useful for the diagnosis and treatment of cancers and immune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Single chain antibody that immunospecifically binds BLyS SeqID 1898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antibody; B lymphocyte stimulator; BLyS; tumour necrosis factor; B cell proliferation; differentiation; scFv; myasthenia gravis; multiple sclerosis; asthma; rheumation arthritis; AIDS; leukaemia; carcinoma; lymphoma; antirheumatic; antiarthritic; neuroprotective; antiinflammatory; antiasthmatic; antiallergic; cytostatic.
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Hilbert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 66; DB 5;
Pred. No. 0.0059;
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Vaughan T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                           Claim 1; Page 2666-2667; 3148pp; English
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Choi GH,
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19-DEC-2001; 2001US-0340817P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 100.
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Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-505530/47.
                                                           WPI; 2002-114799/15.
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   Ruben SM,
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1 SGSTSNIGNNYVS 13
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Best Local Similarity 100.
Matches 13; Conservative
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N-PSDB; ADG34298.
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                                                                                                                                            Local Similarity
es 13; Conserv
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                                                                                                    Sequence 242 AA;
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                                                                         invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
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                                                                                                                                Query Match
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Matches
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ABP45916
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                                                                                                                                                                                          ઠે
                                                  This invention relates to novel antibodies that immunospecifically bind to B lymphocyte stimulator (BLyS). The BLyS gene has been mapped to C chromosome 1344 and encodes a protein that is a member of the tumour necrosis factor superfamily and induces both in vivo and in vitro B cell necrosis factor superfamily and induces both in vivo and in vitro B cell proliferation and differentiation. Specifically, it refers to single chain antibody molecules (GCFWs) derived, preferably, from the variable composition refers to the use of such antibodies in various methods for the detection, diagnosis and prognosis of diseases related to the aberrant expression or inappropriate function of BLyS or its receptor. As such, these compositions are useful for identifying immune disorders including myasthenia gravis and multiple sclerosis, inflammatory disorders e.g. asthma and rheumatorid arthritis, infectious diseases such as AIDS and proliferative disorders including leukaemia, carcinoma and lymphome and confident and the disorders including leukaemia, carcinoma and cymphome. Accordingly, they can be described as exhibiting various cativities such as antirheumatic, antiallergic and cytostatic. This cativities such as antirheumatic, antiallergic and cytostatic. This collypeptide sequence is a single chain antibody that binds BLyS of the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format contine the printed specification, but was obtained in electronic format contined the printed specification, but was obtained in electronic format.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New antibody that specifically binds neurokinin B, useful for preparing a
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       composition for treating or preventing hypertension or preeclampsia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antibody; neurokinin B; hypotensive; gynaecological; gene therapy;
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                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 66; DB 7; Length 240; 100.0%; Pred. No. 0.0059; Pred. No. 0. 10059; ive 0; Mismatches 0; Indels
rheumatoid arthritis, asthma and leukemia.
                             Example 1; SEQ ID NO 1898; 394pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 2; SEQ ID NO 24; 127pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Neurokinin B antibody SEQ ID NO:24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADG34301 standard; protein; 242 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypertension; pre-eclampsia; NKB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       13; Conservative
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ADG34301
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The invention relates to a novel antibody specifically binding neurokinin B. An antibody of the invention has hypotensive, and gynaecological activity, and may have a use in gene therapp. The antibody is useful for preparing a composition for treating or preventing hypotension or preclampsia. The present sequence is used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a novel antibody specifically binding neurokinin B. An antibody of the invention has hypotensive, and gynaecological estivity, and may have a use in gene therapy. The antibody is useful for preparing a composition for treating or preventing hypertension or preciampsia. The present sequence is used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New antibody that specifically binds neurokinin B, useful for preparing a composition for treating or preventing hypertension or preeclampsia.
                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                   100.0%; Score 66; DB 8; Length 242; 100.0%; Pred. No. 0.006; tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                     ilarity 100.0%;
Conservative C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    154 SGSTSNIGNNYVS 166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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Human, protein coordinate data; heavy chain variable domain, VH; cancer; complementarity determining region; CDR; light chain variable domain; VL; TRAIL receptor 7; TR7; tumour necrosis factor; KILLER; death receptor 5; DR5; TRAIL receptor 2; TRAIL-R2; TNF-related apoptosis-inducing ligand; Kaposi's sarcoma; central nervous system; medulloblastoma; neuroblastoma; giloblastoma; graft versus host disease; antibody therapy; nootropic; AlDS; acquired immune deficiency syndrome; neurodegenerative disorder; immunosuppressive; neuroprotective; antibody therapy; antibody.

Human CM085C11 scFv protein that specifically binds TR7

06-OCT-2003 (first entry)

AAO31147;

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BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; fimunosuppressive; immunostimulant; immunomodulatory; antirheumatic; antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency; systemic lupus erythematoeus; rheumatoid arthritis; CVID; AIDS; common variable immunodeficiency; acquired immunodeficiency syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Elymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the tumour necrosis factor (TNF) super family and induces B cell proliferation and differentiation. The antibodies of the invention have cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antirheumatic and antiAlDS activity and can be used in vaccines to inhibit the expression and activity of BLyS. The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in biological samples and may be used in this way to diagnose disease associated with aberrant expression of BLyS. They may also be administered to treat diseases associated with aberrant BLyS expression and activity such as cancer, immune, and autoimmune disorders and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antibodies against B Lymphocyte Stimulating polypeptides, useful for the diagnosis and treatment of cancers and immune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, immunodeficiency (e.g. common variable immunodeficiency (CVID) and acquired immunodeficiency syndrome (AIDS)). ABP43990-ABF47228 represent the antibodies and fragments of the antibodies described in the method of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     invention describes novel antibodies that immunospecifically bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 5; Length 243;
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100.0%; Pred. No. 0.006;
:1ve 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Choi GH, Vaughan T, Hilbert D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1, Page 2700-2701; 3148pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAMBRIDGE ANTIBODY TECHNOLOGY.
                                                                                                                     Human BLyS binding scFv SEQ ID 1927.
ABP45916 standard; protein; 243 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-OCT-2000; 2000US-0240B16P.
16-MAR-2001; 2001US-027624BP.
21-MAR-2001; 2001US-0277379P.
25-MAY-2001; 2001US-029499P.
                                                                                                                                                                                                                                                                                                                                                                                                                     15-JUN-2001; 2001WO-US019110
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                                                                            (first entry)
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Best Local Similarity 100.0
Matches 13, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HUMA-) HUMAN GENOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-114799/15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 243 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-JUN-2000;
                                                                              19-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                              10-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ruben SM,
                                       ABP45916
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                                                                                                                                                                                                                                                                                                 Homo
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Salcedo T, Albert VR, Rosen CA, Humphreys R, Vaughan TJ;

2001US-0341237P. 2002US-0369877P. 2002US-0384828P. 2002US-0396591P.

04-JUN-2002; 20-DEC-2001; 05-APR-2002;

15-AUG-2002; 2002US-0403370P. (HUMA-) HUMAN GENOME SCI INC

19-DEC-2002; 2002WO-US040597

WO2003054216-A2

03-JUL-2003

Homo sapiens

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The invention relates to an isolated antibody or its fragments such as WHCDR1 (heavy chain variable domain complementarity determining region), WHCDR2, WHCDR3, WLCDR3 (light chain variable domain complementarity determining region), VLCDR2 or VLCDR3. The antibody or its fragment immunospecifically binds TRAIL (tumour necrosis factor; TNF-related apoptosis-inducing ligand) receptor 7 (TR7). TR7 is also referred to as TRAIL receptor 2 (TRAIL-R2), death receptor 5 (DR5) and KILLER. The antibody or its fragment is useful for treating, preventing or antibody or its fragment is useful for treating, preventing or gastrointestinal cancer or Kaposi's sarcoma or cancer of the central nervous system such as medulloblastoma, neuroblastoma or glioblastoma or grate, versus host disease, AIDS (acquired immune deficiency syndrome) or a neurodegenerative disease. AIDS (acquired immune deficiency syndrome) or therappy. The present sequence is human scrv protein that specifically
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ameliorating a cancer, e.g. colon, breast, uterine, pancreatic, lu
gastrointestinal cancer, or Kaposi's sarcoma or, graft versus host
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New antibody or its fragment, useful for treating, preventing or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 66; DB 6; Length 243; 100.0%; Pred. No. 0.006; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 2; Page 288; 301pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SGSTSNIGNNYVS 167
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nes 13; Conservative
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N-PSDB; AAL62844.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     disease, AIDS.
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RESULT 15

AA031147 standard; protein; 243 AA.

SGSTSNIGNNYVS 167

155

RESULT 14 AA031147 ID AA03

1 SGSTSNIGNNYVS 13

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Gaps

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Job time : 100.938 secs

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This invention relates to novel antibodies that immunospecifically bind to B lymphocyte stimulator (BLyS). The BLyS gene has been mapped to chromosome 1344 and encodes a protein that is a member of the tumour chromosome 1344 and encodes a protein that is a member of the tumour necrosis factor superfamily and induces both in vivo and in vitro B cell proliferation and differentiation. Specifically, it refers to single chain antibody molecules (scFvs) derived, preferably, from the variable cheavy CDR3 region that immunospecifically bind to a polypeptide, or fragment thereof, of either human, murine, rat or monkey BLyS. The present invention refers to the use of such antibodies in various methods for the detection, diagnosis and prognosis of diseases related to the aberrant expression or inappropriate function of BLyS or its receptor. As such, these compositions are useful for identifying immune disorders cauch, these compositions are useful for identifying immune disorders can including myasthenia gravis and multiple sclerosis, infectious diseases such as ALDS and proliferative disorders including leukaemia, carcinoma and climphoma. Accordingly, they can be described as exhibiting various activities such as antirhemental arthritic, neuroprotective, mission matically and proliferative disorders including antiple such as antirhemental arthritic, neuroprotective, mission mission matically and antiplication of an antiplication and coordingly.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel antibody that immunospecifically binds to a B lymphocyte stimulator (BLys), useful for detecting and treating diseases or disorders e.g. rheumatoid arthritis, asthma and leukemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antiinflammatory, antiasthmatic, antiallergic and cytostatic. This polypeptide sequence is a single chain antibody that binds BLyS of the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format
                                                                                                                                                                       Single chain antibody that immunospecifically binds BLyS SegID 1927.
                                                                                                                                                                                                                   antibody; B lymphocyte stimulator; BLyS; tumour necrosis factor; B cell proliferation; differentiation; scFv; myasthenia gravis; multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia; carcinoma; lymphoma; antirheumatic; antiarthritic; neuroprotective; antiinflammatory; antiasthmatic; antiallergic; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        directely from WIPO at ftp.wipo.int/pub/published pct sequences
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                         ADG96743 standard; protein; 243 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-NOV-2001; 2001US-0331469P.
19-DEC-2001; 2001US-0340817P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-NOV-2002; 2002WO-US036496.
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                                                                                                                          (first entry)
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Best Local Similarity 100...
Best Local 31 Conservative
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                                                                                                                                                                                                                                                                                                                                                                   Unidentified
                                                                                                                          11-MAR-2004
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                                                                            ADG96743;
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100.0%; Score 66; DB 7; Length 243; 100.0%; Pred. No. 0.006; Live 0; Mismatches 0; Indels

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Gaps

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Search completed: October 14, 2005, 16:12:41

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5.1.6
Compugen Ltd.
GenCore version
Copyright (c) 1993 - 2005
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protein search, using sw model OM protein - October 14, 2005, 16:02:59; Search time 18.0781 Seconds (without alignments) 69.190 Million cell updates/sec Run on:

US-10-614-959-13 66

1 SGSTSNIGNNYVS 13 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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80	7	~	7	N	~	7	~	ч	7	7	ч	~	Н	0	~	Н	0	N	7	~	~	7	~	7	~	7	~	0	0
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& Query Match	93.9	93.9	93.9		93.9	93.9	89.4	86.4	84.8		83.3	80.3	80.3			78.8		74.2	72.7	69.7		68.2	68.2	68.2	•	ė.	66.7	66.7	65.9
Score	62	62	62	62	62	62	59	57	26	26	52	53	53	53	53	52	20	49	48	46	45	45	45	45	45	44	44	44	. 43.5
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## ALIGNMENTS

S36050 Ig lambda chain - human (fragment) C;Species Homo sapiens (man) C;Date: 22-Nov-1993 #sequence_revision 01-Dec-1995 #text_change 21-Jan-2000 C;Accession: 836050 R;Williams, S.C. Submitted to the EMBL Data Library, April 1993 A;Reference number: 836046 A;Accession: 836050 A;Residues: preliminary A;Wolecule type: DNA A;Residues: 1-98 <WIL> A;Cross-references: EMBL: 222191; NID: 9312298; PIDN: CAA80201.1; PID: 9312299 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;15-91/Domain: immunoglobulin homology <IMM>

Gape ö Length 98 0; Indels Query Match 93.9%; Score 62; DB 2; Best Local Similarity 92.3%; Pred. No. 0.001; Matches 12; Conservative 1; Mismatches

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1 SGSTSNIGNNYVS 13 ઠે

23 SGSSSNIGNNYVS 35 셤

RESULT 2

847009

19 lambda chain V1-J3 region - human C;Species: Homo sapiens (man) C;Apcession: S47009
R;Mahmoudi, M.; Gasyna, B.; Denomme, G.; Edwards, J.; Bell, D.; Cairns, E. submitted to the EMBL Data Library, July 1994
A;Description: The role of the immunoglobulin heavy chain in human anti-DNA antibody bin A;Reference number: S47009
A;Reference number: S47009
A;Accession: S47009
A;Accession: S47009
A;Molecule type: maNA
A;Molecule type: maNA
A;Molecule type: maNA
A;Residues: 1-111 < WAH>
C;Gypwords: heterotes: EMBL:Z35495; NID:g517346; PIDN:CAA84629.1; PID:g517347
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Superfamily: immunoglobulin homology <IMM>

Gaps ö Length 111; Query Match 93.9%; Score 62; DB 2; Length 111 Best Local Similarity 92.3%; Pred. No. 0.0011; Matches 12; Conservative 1; Mismatches 0; Indels

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1 SGSTSNIGNNYVS 13

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Gaps

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A;Molecule type: mRNA
A;Residues: 1-225. <KKIS.)
A;Cross-references: EMBL:X14583; NID:g33394; PIDN:CAA32725.1; PID:g33395
A;Cross-references: EMBL:X14583; 1899
R;Kishimoto, T.; Okajima, H.; Okumoto, T.; Taniguchi, M.
R;Kishimoto, T.; Okajima, H.; Okumoto, T.; Taniguchi, M.
A;Kishimoto, T.; Okajima, H.; Okumoto, T.; Taniguchi, M.
A;Title: Nucleotide sequences of the cDNAs encoding the V-regions of H- and L-chains of
A;Reference number: S04601; MUID:89296497; PMID:2500644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Hughes-Jones, N.C.; Bye, J.M.; Beale, D.; Coadwell, J.
Biochem. J. 268, 135-140, 1990
Biochem. J. 268, 135-140, 1990
A;Fitle: Nucleotide sequences and three-dimensional modelling of the VH and VL domains A;Reference number: $09710; MUID:90262535; PMID:2111699
A;Accession: $99712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ig lambda chain V region - human
C;Species: Homo sapiens (man)
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
                                                                                                                        A;Cross-references: EMBL:X57806; NID:g33709; PIDN:CAA40944.1; PID:g33710 CS.Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin C;Keywords: heterotetramely F;147-215/Pomain: immunoglobulin homology xIMM>
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A; Residues: 1-130 < KIS2>
A; Residues: 1-130 < KIS2>
A; Cross = references: EMBL:X14583
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
E; 1-20; Domain: signal sequence #statuus predicted < SIG>
F; 1-23; Product: Ig lambda chain #statuus predicted < MAT>
F; 150-218 / Domain: immunoglobulin homology < IMM>
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                    A;Status: preliminary; translation not shown A;Molecule type: mRNA A;Residues: 1-232 <COM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ig lambda chain precursor - human C;Species: Homo sapiens (man) C;Date: 30-Jun-1992 #sequence revi
                                                                                                                                                                                                                                                                                          93.98;
                                                                                                                                                                                                                                                                                                                        92.3%;
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Matches 12; Conserv
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A;Molecule type: mRNA
A;Residues: 1-130 <HUG>
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A;Accession: S25742
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19 lambda chain V region (Zim) - human (fragment)

19 lambda chain V region (Zim) - human (fragment)

19 lambda chain V region (Zim)

19 lambda chain v region (Zim)

19 lambda chain sapiens (man)

19 lambda change 21-Jan-2000

20 lambda c
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Ig lambda chain - human

Ig lambda chain - human

Ig lambda chain - human

C;Species: Homo sapiens (man)

C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000

C;Accession: $25742

C;Accession: $25742

C;Accession: $157312

C;Accession: $1513-1522, 1991

Bur J. Immunol. 21, 1513-1522, 1991

A;Pitle: V(Lambda) and J(Lambda) -C(Lambda) gene segments of the human immunoglobulin lampa;Reference number: $16439; MUID:91257162; PMID:1904362
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Pred. No. 0.0011;
1; Mismatches 0; Indels
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heteroteramer; immunoglobulin
F;14-90/Domain: immunoglobulin homology <IMM>
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Pred. No. 0.0012;
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Best Local Similarity 92.3%;
Matches 12; Conservative
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SGSSSNIGNNYVS 35
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A;Residues: 1-113 <EUL>
C;Superfamily: immunoglob
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Matches 12; Conserv
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C;Accession: S24321
R;Aucouturier, P.; Khamlichi, A.A.; Preud'homme, J.L.; Bauwens, M.; Touchard, G.; Cogne, Biochem. J. 285, 149-152, 1992
A;Title: Complementary DNA sequence of human amyloidogenic immunoglobulin light-chain pr A;Reference number: S24319; MUID:92344562; PMID:1379039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rilanger, B.; Steinmetz-Kayne, M.; Hilschmann, N.
hoppe-Seyler's Z. Physiol. Chem. 349, 345-951, 1968
A.Title: The complete amino acid sequence of Bence-Jones protein New (lambda type). Subg
A.Reference number: A01964; MUID:69060892; PMID:4177823
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A; Map position: 22q11.2-22q11.2
A; Map position: 22q11.2-22q11.2
C; Complex: An immunoglobulin heretoretramer subunit consists of two identical light (kap hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Superfamily: immunoglobulin heretoretramer
F;15-91/Domain: immunoglobulin homology < IMM>
F;22-89/Disulfide bonds: #status predicted
                                                                                                                                                 Ig lambda chain precursor - human
C;Species: Homo sapiens (man)
C;Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
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C;Species: Homo sapiens (man)
C;Accession: Si6048; S36049
R;Williams, S.C.
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C;Species: Homo sapiens (man)
C;Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 09-Jul-2004
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C;Comment: This is a Bence Jones protein.
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Matches 11; Conservative
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nes 10; Conserv
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A,Molecule type: mRNA
A,Residues: 1-131 <AUC>
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A;Map position: 22q11.2-22q11.2
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin predicted <SIG>F;1-19/Domain: signal sequence #status predicted <SIG>F;20-115/Pegion: V segment
F;20-115/Pegion: V segment
F;34-110/Domain: immunoglobulin homology <IMM>F;116-130/Region: J segment
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$47185

Ig lambda chain - human
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C;Accession: $47185
R;McIntcosh, R.S.; Tandon, N.; Metcalfe, R.A.; Weetman, A.P.
R;McIntcosh, R.S.; Tandon, N.; Metcalfe, R.A.; Weetman, A.P.
A;Description: Cloning and analysis of IgM anti-thyroglobulin autoantibodies from patien
A;Reference number: $47181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: UNIPROT:P06316; GB:X01147; NID:g33335; PIDN:CAA25598.1; PID:g758087
C;Genetics:
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Cispecit Homo sapiens (man)

Cispecit Homo sapiens (man)

Cispecit Homo sapiens (man)

Cispecit Homo sapiens (man)

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A;Molecule type: mRNA
A;Residues: 1-111 <MCI>
A;Cross-teferences: EMBL:X79782; NID:g506428; PIDN:CAA56178.1; PID:g506429
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;14-90/Domain: immunoglobulin homology <IMM>
                                                                                    Gaps
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   89.4%; Score 59; DB 2; Length 130; 84.6%; Pred. No. 0.0045;
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Pred. No. 0.01;
2; Mismatches
                                                                            2; Mismatches
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F;41-108/Disulfide bonds: #status predicted
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42 SGTSSNIGNNYVS 54
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Best Local Similarity
Matches 11; Conserva
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A; Molecule type: mRNA
A; Residues: 1-130 <TSU>
                                          Similarity
Query Match
Best Local Simi:
Matches 11;
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Best Local Similarity 83.3
Matches 10; Conservative
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Best Local Similarity
Matches 10; Conserv
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C; Species: Homo sapiens (man)
C; Date: 03-Aug-1984 #sequence_revision 03-Aug-1984 #text_change 09-Jul-2004
C; Species: Homo sapiens (man)
C; Date: 03-Aug-1984 #sequence_revision 03-Aug-1984 #text_change 09-Jul-2004
C; Species: Not 1983
R; Kametani, F.; Takayasu, T.; Suzuki, S.; Shinoda, T.; Okuyama, T.; Shimizu, A.
J; Biochem. 93, 421-429, 1983
A; Title: Comparative studies on the structure of the light chains of human immunoglobuli
A; Reference number: A91970; MUD:83186114; PMID:6404900
A; Rocession: A01965
A; Molecule type: protein
A; Residues: 1-111 < KAM>
A; Rosidues: 1-111 < KAM>
A; Rosidues: 1-111 < KAM>
A; Cross-references: UNIPROT:P01702
C; Genetics:
C; Genetics:
A; Genetics: A; Genetics: C; Genetics: A; Genetics: A; Genetics: C; Genetics: C; Genetics: C; Genetics: A; Genetics: C; Genetics: Genetics: C; Genetics: C; Genetics: Genetics: Genetics: C; Genetics: Genetics: Genetics: C; Genetics: Genetics: Genetics: C; Genetics: Gen
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KResidues: 1-129 cHAR-
A;Cross-references: ENBL:X54446; NID:g37923; PIDN:CAA38313.1; PID:g930121
R;Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Burastero, S.E.; Wilder, R.L.; Notkins
                      A;Reference number: 836046
A;Accession: 836048
A;Status: preliminary
A;Molecule type: DNL
A;Coss-references: EMBL: 222189; NID: 9312294; PIDN: CAA80199.1; PID: 9312295; EMBL: 222190
C;Superfamily: immunoglobulin v region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-91/Domain: immunoglobulin homology < IMM>
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A;Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and patient.
A;Reference number: S23716; MUID:92031262; PMID:1718404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Pred. No. 0.037;
2; Mismatches 0; Indels
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submitted to the EMBL Data Library, April 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80.3%;
76.9%;
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SGSSSNIGSNYV 34
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Matches 10; Conserv
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R; Harindranath, N.
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LIHUNG
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A; Molecule type: mRNA
A; Residues: 1-130 cHAR>
A; Residues: 1-130 cHAR>
A; Cross-references: EMBL:X54438; NID:g37920; PIDN:CAA38307.1; PID:g37921
R; Harindranth, N.; Goldfarb, I.S.; Ikematsu, H.; Burastero, S.E.; Wilder, R.L.; Notkins Int. Immunol. 3, 865-875, 1991
A; Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and l
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C;Date: 19-Nov-1997 #sequence_revision 05-Dec-1997 #text_change 23-Jul-1999
C;Accession: S78057; S23722
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A; Molecule type: mRNA
A; Residues: 19-129 «HAW»
A; Cross-references: EMBL:K54446
C; Superfamily: immunoglobulin V region; immunoglobulin Nomology
C; Keywords: immunoglobulin (fragment) #status predicted «SIG»
F;19-129/Product: ig lambda chain (fragment) #status predicted «SIG»
F;19-129/Product: ig lambda chain (fragment) #status predicted «MAT»
F;33-109/Domain: immunoglobulin homology «IMM»
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A;Residues: 20-130 <HAM-
A;Crose-references: EMBL:X54438
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
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A, Reference number: S23716; MUID: 92031262; PMID: 1718404
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Pred. No. 0.049;
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Pred. No. 0.049;
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A;Reference number: S78051
A;Accession: S78057
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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- protein search, using sw model OM protein October 14, 2005, 15:51:44 ; Search time 86.5312 Seconds (without alignments) 76.932 Million cell updates/sec Run on:

US-10-614-959-13 66 1 SGSTSNIGNNYVS 13 Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

1612378 seqs, 512079187 residues Searched:

Total number of hits satisfying chosen parameters:

1612378

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Query Auch Length DB ID 86.4 130 1 LV1 84.8 101 2 Q8I	DB ID 1 LV10 2 Q8I	ID LV1 OBI	1D LV1G H Q81ZD8	G HUMAN ZD8		
110 2	7 77 77	2 Q81ZD8 2 Q8TE63 1 LV1C HU	OBIECS OBTEGS LVIC HU	MAN		
80.08	10-	2 Q96SB0 1 LV1D HU	096SB0	MAN		
78.8 109 1 1	140	1 LV11 HU	LV11 HU	JAN		
77.3 236 2	101	2 QBNEJ1	Q8NEJ1			
9 74.2 237 2 Q6DHW4 5 68.2 235 2 Q6GMW6	01 00	2 QEDHW4	Q6DHW4		Q6dhw4 homo O6dmw6 homo	o sapien o sapien
66.7 221 2	N	2 Q87LH3	Q87LH3		_	vibrio para
66.7	~ (	2 078035	078035			neurospora
4 66.7 441 Z COUKAZ 3 65.2 1170 Z O7WZN9	N 64	2 QUENTAL	O7WZN9		Qojika puti Q7wzn9 pset	piicilotimaea
.2 1357 2 Q9W4N	2 Q9W4N	2 Q9W4M4	Q9W4M4		-	drosophila
65.2 2186 1 YL52 CAEEL	1 YL52	1 YL52 CAE	YL52 CAE	EL	P34431 caer	caenorhabdi
65.2 2500 2	4 (4	2 096223	096223		_	plasmodium
.6 236 2	N.	2 QGGMV7	Q6GMV7		Oegmv7 homo	homo sapien
2 63.6 348 2 Q97KX3	η,	2 Q97KX3	097KX3	į		clostridium ologination
62.1 111 1	٠,	1 LV6D HUN	TV6D HUN	GAN GAN		sapien
62.1 112 1	-	1 LV1H HUN	LV1H HUN	IAN		sapien
62.1 388 2 Q9VRW7	N	2 Q9VRW7	Q9VRW7		Q9vrw7 dros	drosophila
. 414 1	1 HEM1	1 HEM1_RIC	HEM1_RIC	PR.		rickettsia
62.1 414 2	7	2 Q68VS3	Q68VS3			rickettsia
.1 847 2	ผ	2 Q6BK59	Q6BK59			debaryomyce
.1 958 2	N	2 Q7RRT8	Q7RRT8			plasmodium
62.1 1272 2 Q95SG4	'n	2 Q95SG4	Q95SG4		Q95eg4 dros	drosophila
62.1 1272 2 Q9W117	~	2 09W117	O9W117			drosophila

Q811e2 drosophila Q811a0 drosophila Q811s0 plasmodium P04208 homo sapien P01700 homo sapien Q861b2 photorhabdu O76611 caenorhabdi O8w1r8 lycopersico Q8f125 escherichia Q9f125 escherichia Q9f152 arabidopsis Q47936 francisella Q77967 anopheles P75247 mycoplasma	
Q811E2 Q811A0 Q811A0 Q811S0 LV1F HUMAN LV1B HUMAN LV1B HUMAN Q86FB2 Q96FB2 Q98FIZ5 Q97FZ2 Q47936 Q77EZ9 C1PB_MYCPN	
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## ALIGNMENTS

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib.ch).
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SEQUENCE FROM N.A.
MEDLINE-85662823; PubMed-6095199;
TRUJÍMCIO Y., Croce C.M.;
"Molecular cloning of a human immunoglobulin lambda chain variable
                                                                                            Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606,
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130 130
130 AA, 13564 MW, FA44BBI7D3A55EBF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  86.4%; Score 57; DB 1;
84.6%; Pred. No. 0.069;
rative 2; Mismatches
          HSSP, PO1703, TRAB.

GO; GO:0005576; C:extracellular; NAS.
GO; GO:0005823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-1ike.
InterPro; IPR003596; Ig_v.
SMART; SM00406; IGv; 1.
PR0301E; PS50835; IG_LIKE; 1.
Immnoglobulin V region; Signal.
                                                                                                                                                                                                              sequence.";
Nucleic Acids Res. 12:8407-8414(1984).
                                                                                                                                                                                                                                                                                                                                                     EMBL; X01147; CAA25598.1; -. PIR; A01966; L1HUBL.
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115
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Matches
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1 SGSTSNIGNNYVS 13
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P01701;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
MCBI_TaxID=9606;
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 25, Last annotation update)
10-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Immunglobulin light chain variable region (Fragment).
Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=95007525; PubMed=7923137;
Hall B.L., Murray J.H., Haspel M.V., Kobrin B.J.;
"Establishment, molecular rescue, and expression of 123AV16-1,
tumor-reactive human monoclonal antibody.";
Cancer Res. 54:5178-5185(1994).
EMBL; L33985; AAL68704.1; -.
HSSP; P01703; 7FAB.
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                                                                                                                                                             01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Anti-thyroglobulin light chain variable region (Fragment).
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                                                                                                                                                                                                                                                                                                                                            Jang Y.-J., Chung J., Park J.-Y.;
Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AY145444, AANG4328.1;
HSSP, P01703, 7PAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         101 AA; 10374 MW; 1506C2D9AACBA793 CRC64;
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                                                                                                      101 AA
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InterPro; IPR003596; Ig-v.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR007110; Ig-like.
InterPro; IPR001596; Ig.v.
SMART; SM00406; IGv; 1.
PR00ITE; PS50835; IG_LIKE; 1.
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                                                                                                    PRELIMINARY;
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42 SGSSSNIGNDYVS
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Best Local Similarity
Matches 10; Conserv
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SEQUENCE
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MEDILINE=69060892; PubMed=4177823;
MEDILINE=69060892; PubMed=4177823;
MEDILINE=69060892; PubMed=4177823;
MEDILINE=69060892; PubMed=4177823;
The complete amino acid sequence of Bence Jones protein New (lambda-type). Subgroups in the variable part of immunoglobulin L-chains of the lambda-type.";
The lambda-type.";
The lambda-type.";
The lambda-type.";
S. Physiol. Chem. 349:945-951(1968).
C.-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
PR: AD1703; 7FAB.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0005576; C:extracellular; NAS.
RO; GO:0006955; P:immune response; NAS.
RICERPO; IPR007110; 192-like.
RICERPO; IPR007110; 192-like.
RICERPO; IPR007110; 192-like.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Anti-streptococcal/anti-myosin immunoglobulin lambda light chain
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MEDLINE-98375893; PubMed-9712075;
Adderson E.E., Shikhman A.R., Ward K.E., Cunningham M.W.;
"Molecular analysis of polytractive monoclonal antibodies from rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin
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Pred. No. 0.13;
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SMART; SM00406; IGv; 1.
PR0STTE; PS50615; IG LIKE; 1.
Bence-Jones protein; Direct protein sequencing;
Immunoglobulin V region; Pyrrolidone carboxylic acid.
                                                                                                                                                                                                                                      21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
02-JUL-2004 (Rel. 44, Last annotation update)
1g lambda chain V-I region NEW.
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SGTSSNIGNNEVS 35
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Les 10; Conservative
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Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Aluenner R.D., Collins F.S., Wagner L., Shammen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

HOpkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

La Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Rosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
                                                                                                                                                                                                                                                                         Toft K.G., Sletten K., Husby G.;
"The amino-acid sequence of the variable region of a carbohydrate-containing amyloid fibril protein EPS (immunoglobulin light chain, type lambda).";
                                                                                         Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606,
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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-I- MISCELLANEOUS: Residues 1-2, 56-62, and 74-78 and peptides were positioned by homology.
-I- SIMILARITY. Contains 1 immunoglobulin-like domain.
BIR; A2465, LIHUEP.
HSSP; P01703; 7FAB.
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109 AA; 11414 MW; 556A313E24D5AC73 CRC64;
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N-linked (GlcNAc. ..).
By similarity.
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Last annotation update)
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SMART; SN00406; 1GV; 1.
SMART; SS08085; 1GV; 1.
Amylod; Direct protein sequencing; Glycoprotein; Immunoglobulin V region.
01-JAN-1988 (Rel. 06, Last sequence update) 05-JUL-2004 (Rel. 44, Last annotation update) 1 ambda chain V-I region EPS. Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig-V.
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05-JUL-2004 (TrEMBLrel. 27, Last seq
05-JUL-2004 (TrEMBLrel. 27, Last ann
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wes 10; Conserv
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Name=IGLC2;
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SEQUENCE
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Q6IN99;
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J. Biochem. 93:421-429(1983).
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
PIR; A01965; LiHUWG.
HSSP; P01703; 7FAB.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0003823; F:antigen binding; NAS.
InterPro; IPR0037110; Ig-like.
InterPro; IPR0037110; Ig-like.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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Kametani F., Takayasu T., Suzuki S., Shinoda T., Okuyama T.,
Shimizu A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   80.3%; Score 53; DB 1; Length 111; 76.9%; Pred. No. 0.29;
                                                                                                                                                                                                                                                                                                   80.3%; Score 53; DB 2; Length 108;
83.3%; Pred. No. 0.28;
ive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ig-like.
Pyrrolidone carboxylic acid.
By similarity.
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                                                                                                                                                                                                                                         108 AA; 11594 MW; F4B5DC478A043F48 CRC64;
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SMART: SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
Direct protein sequencing; Immunoglobulin V region;
Pyrrolidone carboxylic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
105-JUL-2004 (Rel. 44, Last annotation update)
11 lambda chain V-I region NIG-64.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                    J. Immunol. 161:2020-2011(1998).
EMBL; U96394; AAB68783.1; -
PDB; IKK4; Model; L=1-108.
InterPro; IPR007110; Ig-like.
InterPro; IPR00356; Ig-v.
SWART; SM00406; IGv; I.
PROSITE; PS50835; IG_LIKE; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LVII_HUMAN
ID LVII HUMAN STANDARD;
AC P0688;
DI 01-JAN-1988 (Rel. 06, Created)
  antibody V region genes.";
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                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 83.3
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 SGSTSNIGNNYVS 13
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                                                                                                                                                                                                                                                                                                                                                                                                                   1 SGSTSNIGNNYV 12
                                                                                                                                                                                                                                                                                                                                                                                                                                             23 SGSSSNIGSNYV 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
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Best Local Similarity
10; Conserva
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SEQUENCE
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SEQÜENCE
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SEQUENCE

RESULT 7

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LV1D_HUMAN

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Gaps

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SEQUENCE FROM N.A.
                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical
SEQUENCE 23
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25-OCT-2004
                                                                                                                                                     TISSUE=Lung
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Q6DHW4
              REPRESENTATION OF THE STATE OF 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakealey R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Strausberg R.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
BEMBL; BC072392; AAH72392.1; -.
HSSP; P010442; 1AQK.
InterPro; IPR003599; Ig.
InterPro; IPR003599; Ig.-Iike.
InterPro; IPR003597; Ig.-Ii.
InterPro; IPR003596; Ig.-Ii.
InterPro; IPR003596; Ig.-V.
Pfam; PR00564; CI-set; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
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SMART; SM00407; IGc1; 1.
SMART; SM00406; IGv; 1.
PROSITE; PSS0035; IG_LIKE; 2.
PROSITE; PS00290; IG_MC; UNKNOWN 1.
SEQUENCE 235 AA; Z4888 MW; 90C95D5E87A6BCC1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                         and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          236 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-0CT-2002 (TrEMBLrel. 22,
01-0CT-2002 (TrEMBLrel. 22,
01-MAR-2004 (TrEMBLrel. 26,
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42 SGRSSNIGNSYVS 54
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Best Local Similarity 76.9
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
TISSUE=Pancreas;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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Q8NEJ1
              SO OR 
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ESUGENCE From A. P. Cells;

XX TISSUB—Frimary B-Cells;

XX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

XI Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

XI Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

XI Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,

XX Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,

XX Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

XX Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

XX Stapleton M.J., Wolin T.B., Toshiyuki S., Carninci P., Prange C.,

XX Raha S.S., Loquellano N.A., Peters G.J., Abrameon R.D., Mullahy S.J.,

XX Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

XX Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

XX Helton B., Ketteman M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,

XX Hakesley X.W., Touchman J.W., Green E.D., Dickson M.C.,

XX Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

XX Jones S.J., Marra M.A.,

XX Jon
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                     Strausberg R.;
Strausberg R.;
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
HESP: PO1703; 7FAB.
InterPro; IPR007110; Ig-1ike.
InterPro; IPR003597; Ig-21.
InterPro; IPR003506; Ig_WHC.
InterPro; IPR003506; Ig_WHC.
R InterPro; IPR003506; Ig_WHC.
R InterPro; IPR003596; Ig_W.
R EMBRT; SM00406; IGv; I.
R SMART; SM00406; IGv; I.
R PROSITE; PS00290; IG_MHC; UNKNOWN_I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC075843; AAH75843.1; -.
InterPro; IPR003599; Ig.
InterPro; IPR00710; Ig-like.
InterPro; IPR003597; Ig_cl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 236 AA; 25024 MW; 1703B77942630E08 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TrEMBLrel. 28, Created)
(TrEMBLrel. 28, Last sequence update)
(TrEMBLrel. 28, Last annotation update)
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 51; DB 2;
Pred. No. 1.3;
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 83.3
Matches 10; Conservative
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087LH3
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Q87LH3
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WEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

A Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

D. Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Guaratane P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Pahey J., Helton E., Ketteman M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

and mouse C.N. Analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                          74.2%; Score 49; DB 2; Length 237; 83.3%; Pred. No. 3; ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Strausberg R.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, BC073784, AAH73784.1; -.
InterPro; IPR001599; Ig.
InterPro; IPR001597; Ig. InterPro; IPR001597; Ig. InterPro; IPR001597; Ig. C1.
InterPro; IPR001506; Ig. MHC.
InterPro; IPR001596; Ig. V.
Pfam; PF00647; Ig. 2.
                                                                                                                                                                                                       Hypothetical protein. - SEQUENCE 237 AA; 25108 MW; 6814170F7E784825 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    235 AA
                                                                                    SMART; SM00409, IG; 2.
SMART; SM00407; IG; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS00290; IG LIKE; 2.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF07654; C1-8et; I.
Pfam; PF00047; ig; 2.
                                                                                                                                                                                                                                                                                             Local Similarity 83.3
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                                                                                                                                                                                                                                                                                                                                                                        1 SGSTSNIGNNYV 12
                                                                                                                                                                                                                                                                                                                                                                                                  42 SGSSSNIGINYV 53
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SMART; SM00407; IGcl; 1.
SMART; SM00406; IGv; 1.
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TISSUE=Primary B-Cells;
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Homo sapiens (Human).
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                                                                                                                                                                                                                                                                               Query Match
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10 GGRWG
10 GGRWG
10 DT 05-JU
DT 05-JU
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DE Hypot
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RX MEDLINE=22508454; PubMed=12620739; DOI=10.1016/S0140-6736(03)12659-1;

RX MEDLINE=22508454; PubMed=12620739; DOI=10.1016/S0140-6736(03)12659-1;

RA Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,

RA Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,

RA Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.,

RI Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism

distinct from that of V. cholerae.";

RI Lancet 361:743-749(2003).

DR GO: GO:0016491; F:oxidoreductase activity; IEA.

GO: GO:0016491; F:oxidoreductase activity; IEA.

GO: GO:0016491; F:oxidoreductase activity; IEA.

DR GO: GO:001852; P:metabolism; IEA.

DR HiterPro; IPR002198; Adh_short_C2.

DR InterPro; IPR002347; Adh_short_C2.

Pfam: PF00106; adh short; 1.
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Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales; Vibrionaceae; Vibrio.
NCBL_TaxID=670;
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                                                                                                                      Length 235;
                                                                                                                                                                        1; Indels
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                                              Hypotherical protein.
SEQUENCE 235 AA; 24803 MW; 058B05F61118F1B8 CRC64;
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Last annotation update)
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Last annotation update)
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66.7%; Pred. No. 20;
11ve 2; Mismatches 2
                                                                                                                      68.2%; Score 45; DB 2; 69.2%; Pred. No. 14;
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                                                                                                                                                                        3; Mismatches
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PROSITE; PS50835; IG_LIKE; 2.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
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01-JUN-2003 (TrEMBLrel. 24, Last seq
01-MAR-2004 (TrEMBLrel. 26, Last ann
Putative short-chain dehydrogenase.
OrderedLocusNames=VP2639;
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01-MAR-2004 (TrEMBLrel. 26,
01-MAR-2004 (TrEMBLrel. 26,
01-MAR-2004 (TrEMBLrel. 26,
Hypothetical protein.
                                                                                             Query Match
Best Local Similarity 69...
Best Local 9; Conservative
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Best Local Similarity 66.7
Matches 8; Conservative
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SEQUENCE 221 AA;
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Search completed: October 14, 2005, 16:19:55 Job time : 88.5312 secs
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A Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B., Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M., Qui D., Ianakiev P., Pedersen D., Nelson M., Washburne M., Schulte U., Schlitzennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U., Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D., A Kamal M., Kamvysselis M., Maucell E., Bleke C., Rudd S., Frishman D., Krystofova S., Rasmussen C., Mezenberg R.L., Perkins D.D., Kroken S., Cogni C., Macino G., Catcheside D., Li W., Pratt R.J., Osmani S.A., DeSouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R., Yarden O., Plamann M., Seller S., Dunlap J., Radford A., Aramayo R., Natvig D.O., Alex. L.A., Mannhaupt G., Ebbolle D.J., Freitag M., Paulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B.; The Genome Sequence of the Filamentous Fungus Neurospora crassa.";
                                                                                                                                                                                                                                                                                                                                                                                                              Nature 0:0-0(2003).
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is preliminary data.

EMBL; AABX01000101; EAA34466.1; -
GO; GO:0005576; C:extracellular; IEA.
GO; GO:0005576; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
GO; GO:0005975; P:carbohydrate metabolism; IEA.
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Viruses; dsDNA viruses, no RNA stage; Baculoviridae; Granulovirus.
NCBI_TaxID=192584;
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Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
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SEQUENCE 326 AA; 33269 MW; 61BC539A292B959F CRC64;
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Late expression factor 4.
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InterPro; IPR05103; GlyCo_hydro_61.
Pfam; PF00734; CBM 1, 1.
Pfam; PF03443; GlyCo_hydro 61; 1.
PROSITE; PS00562; CBD_FUNGAL; 1.
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SEQUENCE 441 AA; 51
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Matches
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08078X
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RESULT 15 Q7WZN9

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PubMed=14983043; DOI=10.1073/pnas.0304622101;
PubMed=14983043; DOI=10.1073/pnas.0304622101;
He J., Baldini R.L., Deziel E., Saucier M., Zhang Q., Liberati N.T.,
Lee D., Urbach J., Goodman H.M., Rahme L.G.;
"The broad host range pathogen Pseudomonas aeruginosa strain PA14
carries two pathogenicity islands harboring plant and animal virulence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
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EMBL; AY273871; AAP81276.1; -
InterPro; IPR008707; Neisseria PilC.
Pfam; PF05567; Neisseria PilC; 1.
SEQUENCE 1170 AA; 128118 MW; 9F4CDF6D681B62F3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
                                                          Last sequence update)
Last annotation update)
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Pred. No. 1.6e+02;
2; Mismatches 1;
PRT; 1170 AA.
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Best Local Similarity 70.00,
PRELIMINARY;
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                                                                                                                                                Pseudomonas aeruginosa
                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                    NCBI_TaxID=287;
                                        01-OCT-2003 (
01-OCT-2003 (
01-MAR-2004 (
                                                                                                                              Name=pilY1;
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SGSTSNIGNNYVS 13
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US-09-383-667-13
US-08-665-202-37
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                                                      October 14, 2005, 16:00:04; Search time 25.5938 Seconds (without alignments) 37.917 Million cell updates/sec
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Sequence 4
Sequence 4
Sequence 3
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1: /cgn2_6/ptodata1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata1/iaa/PCTUS_COMB.pep:*
         5.1.6
Compugen Ltd.
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US-08-665-202-37

US-08-665-202-42

US-08-665-202-43

US-08-665-202-43

US-08-665-202-43

US-08-665-202-43

US-08-983-607-35

US-09-315-574-43

US-09-315-574-43

US-09-315-574-43

US-09-315-574-43

US-09-315-574-39

US-09-490-15-18

US-09-490-15-18

US-09-490-15-18

US-09-490-15-18

US-09-490-15-18

US-09-490-15-18

US-09-315-574-5

US-09-315-574-7
                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                              513545 segs, 74649064 residues
         GenCore version (c) 1993 - 2005
                                                                                                                                                                                                                                                                                                                                       SUMMARIES
                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                       - protein search, using sw model
                                                                                                                       BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                       1 SGSTSNIGNNYVS 13
                                                                                                                                                                               length: 0
length: 2000000000
                                                                                       US-10-614-959-13
66
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Match Length
                Copyright
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seg
                                                                                                                       Scoring table:
                                                                                                Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                               Minimum DB
Maximum DB
                                       OM protein
                                                                                                        Sequence:
                                                                                                                                                Searched:
                                                                                                                                                                                                                                        Database
                                                        Run on:
                                                                                                                                                                                                                                                                                                                                                      Result
No.
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93.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23 SGSSSNIGNNYVS 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 93.9
Best Local Similarity 92.3
Matches 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-665-202-36
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Patent No. 6512097
GENERAL INFORMATION:
APPLICANT: Marks, James D.
APPLICANT: Schier, Robert
TITLE OF INVENTION: No. 6512097e1 High Affinity Human Antibodies to TINUER OF INVENTION: Tumor Antigens
NUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 62; DB 2; Length 98;
Pred. No. 0.007;
1; Mismatches 0; Indels
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STREET: Four Embarcadero Center, Suite 1100
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-4106
COMPUTER READBALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/315,574
FILING DATE: 20-MAY-99
CLASSIFICATION: 530
                                   COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,202
FILING DATE: 13-JUN-1996
FILING DATE: 14-JUN-1996
PRIOR APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
PRIOR APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
ATPORNEY/AGENT INFORMATION:
APPLICATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 35,498
REFERENCE/DOCKET NUMBER: 35,498
REFERENCE/DOCKET NUMBER: 35,498
REFERENCE/DOCKET NUMBER: 37:
TELEPHONE: (415) 576-0300
INPORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-UN-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23 SGSSSNIGNNYVS 35
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Best Local Similarity 92.3
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-665-202-37
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-315-574-37
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US-08-665-202-302-30

US-08-665-202-30

US-08-665-202-30

US-08-665-202-30

US-08-665-202-30

UNUMERATION: Mo. 59773221 High Affinity Human Antibodies to TITLE OF INVENTION: No. 59773221 High Affinity Human Antibodies to TITLE OF INVENTION: No. 59773221 High Affinity Human Antibodies to TITLE OF INVENTION: No. 59773221 High Affinity Human Antibodies to TITLE OF INVENTION: Thunc Antigens

UNUMERS OF SEQUENCES: 141

CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco

STATE: California

CONTRY: USA

ZIP: 9411-384

COMPTER: USA

COMPTER: ISP COMPATIBLE

COMPUTER: ISP COMPATIBLE

COMPUTER: ISP COMPATIBLE

COMPUTER: ISP COMPATIBLE

COMPUTER: USA

CORRENT APPLICATION DATA: APPLICATION NUMBER: US 60/000, 238

FILLING DATE: 13-UTN-1995

RELING APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: US 60/000, 250

FILLING DATE: 13-UTN-1995

RELING APPLICATION NUMBER: US 60/000, 250

FILLING DATE: 13-UTN-1995

RESTRUCTION NUMBER: US 60/000, 250

FILLING DATE: 13-UTN-1995

RESTRUCTION NUMBER: US 60/000, 250

FILLING DATE: 13-UTN-1995

RESTRUCTION NUMBER: US 60/000, 250

REAL HUMBER: USA

RESTRUCTION NUMBER: USA

NAME: HUMLEY, TOM

REFERENCE/DOCKET NUMBER: 033078-061410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Pred. No. 0.007;
1; Mismatches 0; Indels
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/665,202
FILING DATE: 13-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: HUNCEY, TOM
REGISTRATION NUMBER: 38,498
REPERRENCE/DCKET NUMBER: 03307E-061411
TELECHONNICATION INFORMATION:
TELECHONEY (415) 576-0200
INFORMATION FOR SEQ ID NO: 37:
LENGTH: 98 amino acide
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TELECOMMINICATION INFORMATION:
TELEFAX: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
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RESULT 7
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Patent No. 5977322

GENERAL INFORMATION:

APPLICANT: Marks, James D.

APPLICANT: Schier, Robert

TITLE OF INVENTION: No. 5977322el High Affinity Human Antibodies to

TITLE OF INVENTION: No. 5977322el High Affinity Human Antibodies to

TITLE OF INVENTION: No. 5977322el High Affinity Human Antibodies to

TITLE OF INVENTION: No. 5977322el High Affinity Human Antibodies to

TITLE OF INVENTION: No. 5977322el High Affinity Human Antibodies to

TITLE OF INVENTION: No. 5977322el High Affinity Human Antibodies to

TITLE OF INVENTION: Ample ADMESS:

ADDRESSER: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco

STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco

STREET: Two Embarcadero Center, Eighth Floor

STREET: Ban Prancisco

STREET: Two Embarcadero Center, Eighth Floor

STREET: Ban Procompatible

COMPUTER: READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Plan Procompatible

COMPUTER: Plan Procompatible

COMPUTER: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION NUMBER: US 60/000, 238

FILING DATE: 13-JUN-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/000, 250

FILING DATE: 15-JUN-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/000, 250

FILING DATE: 15-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: HUMBER: Town NUMBER: US 60/000, 250

FILING DATE: NUMBER: US 60/000, 250

FILING DATE: NUMBER: US 60/000, 250
                                                                                                                                                                                                Gaps
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                                                                                                                                    93.9%; Score 62; DB 2; Length 111; 92.3%; Pred. No. 0.0079; Live 1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061410
TELECOMNUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0300
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
ILENGTH: 111 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                               23 SGSSSNIGNNYVS 35
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                                                                                                                                                                                             12; Conservative
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; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-665-202-36
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                                                                                                                                                           Best Local Similarity
Matches 12; Conserv
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Best Local Similarity
Matches 12; Conserva
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US-08-665-202-42
                                                                                                                                       Query Match
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Sequence 43, Application US/08665202
Patent No. 5977322
GENERAL INFORMATION:
APPLICANT: Marks, James D.
APPLICANT: Schier, Robert
TITLE OF INVENTION: Tumor Antigens
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS: 41
CORRESPONDENCE ADDRESS: STREET: Townsend and Townsend and Crew LLP
STREET: Townsend and Townsend and Crew LLP
STREET: ADDRESSE: Townsend and Townsend and Crew LLP
STREET: ALO Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Sequence 35, Application US/08983607

GENERAL INFORMATION:
APPLICANT: Alandong Cai
TITLE OF INVENTION: Human Anti-Tumor Monoclonal Anti-
TITLE OF INVENTION: bodies
NUMBER OF SEQUENCES: 51

CORRESPONDENCE ADDRESS:
ADDRESSEE: Department of Molecular Biophysics
ADDRESSEE: and Blochemistry, Yale University
STREET: 266 Whitney Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 62; DB 2; Length 111 Pred. No. 0.0079; 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUW TYER: EIBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,202
FILING DATE: 13-JUN-1996
CLASSIFICATION: 424
PRIOR APPLICATION HATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
PILING APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
ATPONEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 38,498
REFERENCE/COCKET NUMBER: 38,498
REFERENCE/COCKET NUMBER: 376-0200
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION TELECOMMUNICATION TELECOMUNICATION TELECOMMUNICATION TE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RY: United States of America 06520-8114
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Best Local Similarity 92.3%;
Matches 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; MOLECULE TYPE: peptide US-08-665-202-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: Unit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
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A STATE OF

RESULT 6 US-08-665-202-43

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USA
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Sequence 36, Application US/09315574

GENERAL INFORMATION:

APPLICANT: Schier, Nobert

TITLE OF INVENTION: Twoor Antigens

TITLE OF INVENTION: Twoor Antigens

NUMBER OF SEQUENCES: 141

CORRESPONDENCE ADDRESS:

ADDRESSEE: Majestic, Parsons, Siebert & Hsue P.C.

STREST: California

COUNTRY: USA

IP: 94111-4106

CONPUTER: Eloppy disk

COMPUTER: IBM PC compatible

COMPUTER: PATENTIS PC-DOS/MS-DOS

SOFTWARE: PATENTIN Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/315,574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Pred. No. 0.0079;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens (melanoma patient immu-ORGANISM: nized with autologous tumor cells) INDIVIDUAL ISOLATE: peripheral blood lymphocytes IMMEDIATE SOURCE: LIBRARY: EUSES fusion phage construct CLONE: V373
                                  COMPUTER: IBM PC
COMPUTER: IBM PC
SOFTWARE: Word Processing
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/983,607
FILING DATE: APTI1 27, 1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/IB96/01032
FILING DATE: June 28, 1996
CLASSIFICATION: 435
ATTONNEY/AGENT INFORMATION:
NAME: MATY M. KTINEKY
REGISTRATION NUMBER: 32423
REFERENCE/DOCKET NUMBER: 0CR-679
TELEFON. 203-773-183
INFORMATION FOR SEQ ID NO: 35:
ELENGTH: 111 residues
TTELETAX: 203-773-183
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 111 residues
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE:
DESCRIPTION: polypeptide
ORIGINAL SOURCE:
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" 1.44 Mb diskette
COMPUTER: IBM PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93.9%;
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Best Local Similarity 92.3
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; NAME/KEY: light chain US-08-983-607-35
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US-09-315-574-36
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PRIOR APPLICATION NATA:

APPLICATION NATE:

APPLICATION NATE:

APPLICATION NATE:

PRIOR APPLICATION NATE:

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US-09-315-574-43

| US-09-315-574-43
| Sequence 43, Application US/09315574
| Patent No. 6512097
| GENERAL INFORMATION:
| APPLICANT: Marks, James D. APPLICANT: Schier, Robert
| TITLE OF INVENTION: No. 6512097el High Affinity Human Antibodies to TITLE OF INVENTION: Tumor Antigens
| WUMBER OF SEQUENCES: 141
| CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                           Score 62, DB 4; Length 111;
Pred. No. 0.0079;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FOCOMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/315,574
FILING DATE: 20-MAY-99
CLASSIFICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
FILING DATE: 13-JUN-1995
PRIOR APPLICATION NUMBER: US 60/665,202
FILING DATE: 13-JUN-1996
ATTORNEY/ARENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Majestic, Parsons, Siebert & Heue P.C. STREET: Four Embarcadero Center, Suite 1100 CITY: San Francisco STATE: California
REGISTRATION NUMBER: 38,498
REPERENCE/DOCKET NUMBER: 02307E-061411
TELECOMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Hunter, Tom
REGISTRATION UNMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061411
TELECOMNUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                93.9%;
                                                                                                                                                                       LENGTH: 111 amino acids
TYPE: amino acid
STRANDEDNESS:
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TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                            1 SCSTSNIGNNYVS 13
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                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 92.3
Matches 12; Conservative
                                                                                                                                                                                                                                              ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-315-574-42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: peptide
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US-08-665-202-39
US-08-665-202-39
Sequence 39, Application US/08665202
Patent No. 5977322
GENERAL INFORMATION:
APPLICANT: Marks, James D.
TITLE OF INVENTION: No. 5977322el High Affinity Human Antibodies to TITLE OF INVENTION: No. 5977322el High Affinity Human Antibodies to TITLE OF INVENTION: No. 5977322el High Affinity Human Antibodies to TITLE OF INVENTION: No. 5977322el High Affinity Human Antibodies to TITLE OF INVENTION: No. 597732el High Affinity Human Antibodies to TITLE OF INVENTION: Than Antibodies to TITLE OF INVENTION: Antibodies to TITLE OF INVENTION: Antibodies to TITLE OF INVENTION: ANTIBODIES:
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
CITY: California
                                                              Gaps
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                   Length 111;
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              Score 62; DB 4; Length 111
Pred. No. 0.0079;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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ZIP: 94111-3834

ZOUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,202
FILING DATE: 13-UTN 1996
CLASSIFICATION 1424
PRIOR APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
PRIOR APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
ATPONEY/ARET INFORMATION:
NAME: MARKET NUMBER: US 60/000,250
FILING DATE: THORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 62; DB 2;
Pred. No. 0.008;
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 0230
TELECOMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
INFORMATION FOR SEQ ID NO: 39: SEQUENCE CHARACTERISTICS:
LENGTH 112 amino acide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 93.9%;
Best Local Similarity 92.3%;
Matches 12; Conservative
Query Match
Best Local Similarity 92.3
                                                                                                                                     23 SGSSSNIGNNYVS 35
                                                                                                        1 SGSTSNIGNNYVS 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Alan Garen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid STRANDEDNESS:
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RESULT 14
US-09-315-574-39
i Sequence 39, Application US/09315574
j Patent No. 6512097
GENERAL INFORMATION:
APPLICANT: Marks, James D.
APPLICANT: Schier, Robert
TITLE OF INVENTION: Tumor Antigens
NUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESS:
ADDRESSEE: Majestic, Parsons, Siebert & Hsue P.C.
STREET: Four Embarcadero Center, Suite 1100
STREET: California
COUNTRY: USA
STAIL: All of Campacible
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compacible
OPERATING SYSTEM: PC-DoS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CLASSIFCATION DATA:
PRILICATION NUMBER: US/09/315,574
FILING DATE: 14-UUN-1995
FILING DATE: 14-UUN-1995
                                                                                                                                                                                                                   COMPUTER FRADABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OMPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn PC-Base #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION NUMBER: BP 95 11 3021.0
FILING DATE: 18-MG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: WORPHO/5
FILING DATE: 1215,596-9000
TELECOMMUNICATION INFORMATION:
TELEPRAX: (212)596-9000
TELEPRAX: (212)596-9000
TELEPRAX: (212)596-9000
INPORMATION POR SEQ ID NO: 18:
SEQUENCE TRRACTERISTICS:
LENGTH: 112 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 62; DB 3; Length 112;
Pred. No. 0.008;
                               CORRESPONDENCE ADDRESS:
ADDRESSEB: James F. Haley, Jr., Esq. c/o Fish & Neave STREET: 1251 Avenue of the Americas CITY: New York STATE: New York COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
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Best Local Similarity 92.39
Matches 12; Conservative
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MOLECULE TYPE: protein
         TUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-025-769B-18
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Pred. No. 0.008;
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APPLICANT: Xiaohong Cai
TITLE OF INVENTION: Human Anti-Tumor Monoclonal Anti-
TITLE OF INVENTION: bodies
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Department of Molecular Biophysics
ADDRESSEE: and Biochemistry, Yale University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 18, Application US/09025769B
Patent No. 6300064
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Raappik, Achim
APPLICANT: 1189, Vic
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plucekthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens (melanoma patient immu-
ORGANISM: nized with autologous tumor cells)
INDIVIDUAL ISOLATE: peripheral blood lymphocytes
IMMEDIATE SOURCE:
ILIBRARY: DM414 scFv antibodies obtained from
ILIBRARY: fUSE5 fusion phage construct
CLONE: V73
                                                                                                                                                                          ADDRESSEE: and Biochemistry, Yale Unive STREET: 266 Whitney Avenue
CITY: New Haven
STATE: Connection
CONNTRY: United States of America
ZIP: 06520-814
COMPUTER: BAP PC
COMPUTER: 15M PC
CLASSIFICATION NUMBER: DCT/1896/01032
FILING DATE: June 28, 1996
CLASSIFICATION NUMBER: 32423
REFERENCE/DOCKET NUMBER: 32423
REFERENCE/DOCKET NUMBER: 3243
REFERENCE/DOC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 93.9%;
Best Local Similarity 92.3%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE:
DESCRIPTION: polypeptide
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 SGSTSNIGNNYVS 13
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Gaps

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PRIOR APPLICATION DATE:

APPLICATION NUMBER: US 60/000,250
FRICK PAPLICATION NUMBER: US 05/000,250
FRICK PAPLICATION NUMBER: US 05/000,250
ATTODING VARIET HINDONITION NUMBER: 03/496
RESTRANTON NUMBER:
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JS-09-880-748-1898
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LENGTH: 240
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Sequence 1898, Ap
Sequence 24, Appl
Sequence 40, Appl
Sequence 53, Appl
Sequence 1927, Ap
Sequence 29, Appl
Sequence 29, Appl
Sequence 31, Appl
Sequence 53, Appl
Sequence 53, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                         October 14, 2005, 16:20:10 ; Search time 92.4219 Seconds (without alignments) 58.615 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Published Applications AA:*

| cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/USO6_PUB_OPD:*
4: /cgn2_6/ptodata/2/pubpaa/USO6_PUB_OPD:*
5: /cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/USO06_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/USO06_PUBCOMB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/USO06_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/USO06_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/USO06_PUBCOMB.pep:*
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18: /cgn2_6/ptodata/2/pubpaa/USO06_PUBCOMB.pep:*
19: /cgn2_6/ptodata/2/pubpaa/USO06_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/USO06_PUBCOMB.pep:*
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US-10-981-692-24
US-10-981-692-40
US-10-181-692-10
US-10-193-418-1927
US-10-981-692-29
US-10-981-692-33
US-10-981-465-53
US-10-981-465-53
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GenCore version (c) 1993 - 2005
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Maximum Match 100%
Listing first 45 summaries
                                                                                    protein search, using sw model
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1926, Ap
1926, Ap
3241, Ap
31, Appl
36, Appl
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46, Appl
88, Appl
27, Appl
37, Appl
44, Appl
39, Appl
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Sequence 8
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          Sequence
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US-10-981-691-53

US-10-981-691-53

US-10-293-418-1926

US-10-293-418-1926

US-10-293-418-1926

US-10-293-418-1913

US-09-880-748-1913

US-09-880-748-1913

US-09-880-748-1913

US-09-880-748-1928

US-10-293-418-1934

US-10-293-418-1934

US-10-293-418-1928

US-10-293-418-1928

US-10-293-418-1928

US-10-293-418-1928

US-10-293-418-1928

US-10-293-418-1928

US-10-293-418-1928

US-10-293-418-1928

US-10-981-692-37

US-11-046-857-44

US-10-981-692-39

US-09-880-748-1618
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## ALIGNMENTS

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Gaps
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US-09-880-748-1898
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1 SGSTSNIGNNYVS 13

153 SGSTSNIGNNYVS 165

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US-10-981-632-24
i Sequence 24, Application US/10981692
i Publication No. US20050163777A1
i GENERAL INFORMATION:
i APPLICANT: Rosen et al.
i TITLE OF INVERTION: Antibodies that Specifically Bind to Neurokinin B
i TITLE OF INVERTION NUMBER: US/10/981,692
i CURRENT FILING DATE: 2004-11-05
i PRIOR FILING DATE: 2003-05-29
i PRIOR FILING DATE: 2003-05-29
i PRIOR FILING DATE: 2002-05-30
i NUMBER OF SEQ ID NOS: 76
i SOFTWARE: PatentIn version 3.1
i SEQ ID NO 24
i EMEGTH: 242
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OTHER INFORMATION: N015E08 BCFV

US-10-981-692-24
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Best Local Similarity 100.(
Matches 13; Conservative
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ORGANISM: Homo sapiens
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TITLE OF INVENTION: Antibodies that Specifically Bind to Neurokinin B FILE REFERENCE: PFS0PD1

CURRENT APPLICATION NUMBER: US/10/981,692

CURRENT FILING DATE: 2004-11-05

PRIOR FILING DATE: 2003-05-29

PRIOR FILING DATE: 2003-05-29

PRIOR FILING DATE: 2002-05-30

NUMBER OF SEQ ID NOS: 76

SOFTWARE: Patentin version 3.1

SEQ ID NO 40

LENGTH: 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ## Sequence 1927, Application US/09880748
## Publication No. US20030059937A1
| GENERAL INFORMATION:
| APPLICANT: Ruben et al. |
| TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
| TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
| TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
| TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
| CURRENT APPLICATION NUMBER: 60/212,210
| RIOR APPLICATION NUMBER: 60/212,210
| RIOR PILING DATE: 2000-10-17
| RIOR PILING DATE: 2000-10-17
| RIOR APPLICATION NUMBER: 60/276,248
| PRIOR PILING DATE: 2001-03-16
| PRIOR PILING DATE: 2001-03-21
| PRIOR PILING DATE: 2001-05-25
| NUMBER OF SEQ ID NOS: 3239
| SEQ ID NOS: 3239
| SEQ ID NO 1927
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100.0%; Pred. No. 0.007;
ative 0; Mismatches 0;
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; Sequence 40, Application US/10981692
; Publication No. US20050163777A1
; GENERAL INFORMATION:
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US-10-981-692-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial sequence
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                  154 SGSTSNIGNNYVS 166
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Best Local Similarity 100.
Matches 13; Conservative
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; ORGANISM: Homo sapiens
US-09-880-748-1927
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Matches 13; Conserva
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US-09-880-748-1927
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CTHER INFORMATION: N023E01 scFv
US-10-981-692-33
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US-10-981-692-29
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Best Local Similarity 100.0%;
Matches 13; Conservative 0
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ORGANISM: Artificial sequence
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TYPE: PRT
COGGANISM: Artificial sequence
FEATURE:
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; ORGANISM: Homo sapiens
US-10-293-418-1927
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                                                                                          Sequence 53, Application US/1032673

Sequence 53, Application US/1032673

Publication No. US20030180296A1

GENERAL INFORMATION:

APPLICANT: Salcede tal.

TITLE OF INVENTION: Receptors

FILE OF INVENTION NUMBER: US/10/32,673

CURRENT APPLICATION NUMBER: 60/341,237

FRIOR FILING DATE: 2002-12-20

FRIOR FILING DATE: 2002-06-04

FRIOR FILING DATE: 2002-06-04

FRIOR FILING DATE: 2002-06-18

FRIOR FILING DATE: 2002-01-18

FRIOR FILING DATE: 2002-11-13

NUMBER 0F SEQ ID NOS: 72

FRIOR FILING DATE: 2002-11-13
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Sequence 1927, Application No. US2030322396A1

GENERAL INFORMATION:

APPLICATY: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REFERENCE: PF5232

CURRENT APPLICATION NUMBER: US/10/293,418

CURRENT FILING DATE: 2002-11-27

PRIOR APPLICATION NUMBER: 60/314,69

PRIOR FILING DATE: 2001-11-6

PRIOR FILING DATE: 2001-6-15

PRIOR FILING DATE: 2001-06-15

PRIOR FILING DATE: 2001-06-15

PRIOR PILING DATE: 2001-06-25

PRIOR PILING DATE: 2001-06-25

PRIOR PILING DATE: 2001-06-25

PRIOR PILING DATE: 2001-01-6-15

PRIOR PILING DATE: 2001-01-6-15

PRIOR PILING DATE: 2001-01-6-16

PRIOR FILING DATE: 2001-01-6-16

PRIOR FILING DATE: 2001-01-17

PRIOR PILING DATE: 2001-01-17

PRIOR PILING DATE: 2000-01-17

PRIOR PILING DATE: 2000-01-17

PRIOR PILING DATE: 2000-06-16

PRIOR FILING DATE: 2000-06-16

PRIOR FILING DATE: 2000-06-16

PRIOR FILING DATE: 2000-06-16

NUMBER OF SEQ ID NOS: 3247

TANDE: DENTE DATE: 2000-06-16

SEQ ID NO 1927
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100.0%; Score 66; DB 14; Length 243;
Best Local Similarity 100.0%; Pred. No. 0.007;
Matches 13; Conservative 0; Mismatches 0; Indels 0
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COTHER INFORMATION: CM085C11 SCFVUS-10-322-673-53
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ORGANISM: Artificial sequence
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US-10-981-692-33

Sequence 33, Application US/10981692

Publication No. US2005016377A1

GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: Antibodies that Specifically Bind to Neurokinin B

FILE REFERENCE: PFS90P1

CURRENT APPLICATION NUMBER: US/10/981,692

CURRENT FILING DATE: 2004-11-05

FRIOR FILING DATE: 2003-05-29

PRIOR FILING DATE: 2003-05-30

PRIOR FILING DATE: 2003-05-30

NUMBER: PEQ 1D NOS: 76

SOFTWARE: PatentIn version 3.1

SEQ ID NO 33

LENGTH: 243
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| Sequence 29, Application US/20050163777A1
| Sequence 29, Application No. US20050163777A1
| GENERAL INFORMATION:
| APPLICANT: ROSEN et al. |
| TITLE OF INVENTION: Antibodies that Specifically Bind to Neurokinin B
| FILE REFERENCE: PF590P1 |
| CURRENT APPLICATION NUMBER: US/10/981,692 |
| CURRENT FILING DATE: 2004-11-05 |
| PRIOR APPLICATION NUMBER: 60/383,802 |
| PRIOR APPLICATION NUMBER: 60/383,802 |
| PRIOR PRILING DATE: 2002-05-30 |
| RATOR FILING DATE: 2002-05-30 |
| NUMBER OF SEQ ID NOS: 76 |
| SEQ ID NO SEQ ID NOS: 76 |
| SEQ ID NO SEQ ID NOS: 76 |
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| SEQ ID NO SEQ ID NOS: 76 |
| SEQ ID NO SEQ ID NOS TO SEQ ID NOS TO SEQ ID NO SEQ
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100.0%; Score 66; DB 18; Length 243;
Best Local Similarity 100.0%; Pred. No. 0.007;
Matches 13; Conservative 0; Mismatches 0; Indels (
Query Match
100.0%; Score 66; DB 15; Length 243;
Best Local Similarity 100.0%; Pred. No. 0.007;
Matches 13; Conservative 0; Mismatches 0; Indels C
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Pred. No. 0.007;
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TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
TITLE OF INVENTION: Receptors
FILE REFERENCE: PF585P102
CURRENT APPLICATION NUMBER: 60/608,386
PRIOR FILING DATE: 2004-09-10
PRIOR PRILING DATE: 2004-09-10
PRIOR PILING DATE: 2003-06-15
PRIOR PRILING DATE: 2003-66-15
PRIOR PRILING DATE: 2003-66-15
PRIOR PRILING DATE: 2002-04-15
PRIOR PILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: 60/396,591
PRIOR PILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: 60/403,370
PRIOR APPLICATION NUMBER: 60/405,737
PRIOR PRILING DATE: 2002-01-18
PRIOR PILING DATE: 2002-01-18
PRIOR PRILING DATE: 2002-01-18
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NUMBER OF SEQ ID NOS: 76
SEQ ID NO 53
LENGTH: 243
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PRIOR FILING DATE: 2003-08-15
PRIOR APPLICATION NUMBER: 10/322,673
PRIOR FILING DATE: 2002-12-19
PRIOR APPLICATION NUMBER: 60/369,877
PRIOR FILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: 60/384,828
PRIOR APPLICATION NUMBER: 60/396,591
PRIOR APPLICATION NUMBER: 60/403,370
PRIOR FILING DATE: 2002-07-18
PRIOR PELING DATE: 2002-07-18
PRIOR PELING DATE: 2002-08-15
PRIOR FILING DATE: 2002-08-15
PRIOR PELING DATE: 2002-08-15
PRIOR PELING DATE: 2002-08-15
PRIOR PELING DATE: 2002-01-13
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ORGANISM: Artificial sequence
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TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
TITLE OF INVENTION: Receptors
FILE REFERENCE: PF5851
CURRENT FILING DATE: 2004-01-05
PRIOR PILING DATE: 2004-09-10
PRIOR PILING DATE: 2004-09-10
PRIOR PILING DATE: 2004-05-06
PRIOR FILING DATE: 2003-05-06
PRIOR FILING DATE: 2003-05-06
PRIOR PILING DATE: 2003-05-06
PRIOR PILING DATE: 2003-06-06
PRIOR PILING DATE: 2002-06-06
PRIOR PILING DATE: 2002-06-16
PRIOR PILING DATE: 2002-11-13
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Sequence 53, Application US/10981621

Sequence 53, Application No. US20050214206A1

GENERAL INFORMATION:

TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL

TITLE OF INVENTION: Receptors

FILE REFERENCE: PFS8F1D1

CURRENT APPLICATION NUMBER: US/10/981,621

CURRENT FILING DATE: 2004-10-5

PRIOR FILING DATE: 2004-09-10

PRIOR PLING DATE: 2004-09-10

PRIOR APPLICATION NUMBER: 60/68,386

PRIOR FILING DATE: 2004-09-10

PRIOR PLING DATE: 2004-09-0

PRIOR FILING DATE: 2003-05-05

PRIOR FILING DATE: 2003-05-06

PRIOR FILING DATE: 2003-05-06

PRIOR FILING DATE: 2003-05-06

PRIOR FILING DATE: 2003-05-06

PRIOR APPLICATION NUMBER: 60/495,140
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; Sequence 53, Application US/10981465
; Publication No. US20050214205A1
; GENERAL INFORMATION:
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US-09-880-748-1926
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US-10-981-692-26
US-10-981-692-26
Sequence 26, Application US/10981692
Publication No. US20050163777A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVERTION: Antibodies that Specifically Bind to Neurokinin B
TILE REFERENCE: PFS-90P1
CURRENT APPLICATION NUMBER: US/10/981,692
CURRENT FILING DATE: 2004-11-05
PRIOR APPLICATION NUMBER: PCT/US03/16802
PRIOR APPLICATION NUMBER: 60/383,802
PRIOR FILING DATE: 2002-05-30
                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:

TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL

TITLE OF INVENTION: Receptors

FILE REFERENCE: PF565P1D3

CURRENT PAPLICATION NUMBER: US/10/981,691

CURRENT TILING DATE: 2004-11-05

PRIOR APPLICATION NUMBER: 60/608,386

PRIOR FILING DATE: 2004-09-10

PRIOR FILING DATE: 2004-09-0

PRIOR FILING DATE: 2004-05-05

PRIOR FILING DATE: 2003-05-06

PRIOR FILING DATE: 2003-04-05

PRIOR FILING DATE: 2002-04-05

PRIOR FILING DATE: 2002-07-18

PRIOR PLING DATE: 2002-07-18

PRIOR PLING DATE: 2002-07-18

PRIOR FILING DATE: 2002-07-18

PRIOR FILING DATE: 2002-07-18

PRIOR FILING DATE: 2002-08-15

PRIOR FILING DATE: 2002-01-18

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  100.0%; Score 66; DB 18; Length 243; 100.0%; Pred. No. 0.007; tive 0; Mismatches 0; Indels
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ORGANISM: Artificial sequence
                                                                                                                                                                           155 SGSTSNIGNNYVS 167
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Query Match
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                                                                ; OTHER INFORMATION: N024D01 scFv
US-10-981-692-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%;
           PatentIn version 3.1
                                        TYPE: PRT ORGANISM: Artificial sequence
                                                                                                                                                      156 SGSTSNIGNNYVS 168
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                                                                                                                                         1 SGSTSNIGNNYVS 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 13; Conservative
NUMBER OF SEQ ID NOS: 76
SOFTWARE: PatentIn versic
SEQ ID NO 26
LENGTH: 244
                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1926
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Compugen Ltd.
GenCore version (c) 1993 - 2005
           Copyright
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- protein search, using sw model OM protein

Run on:

October 14, 2005, 15:51:19; Search time 53.8125 Seconds (without alignments) 50.310 Million cell updates/sec

US-10-614-959-14 35 score:

1 DVSKRPS 7 Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

2105692 seqs, 386760381 residues Searched:

2105692 Total number of hits satisfying chosen parameters:

Minimum DB Maximum DB

seq length: 0 seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* geneseqp2004s:* A_Geneseq_16Dec04:* geneseqp1980s:* geneseqp1990s:* geneseqp2000s:* geneseqp2001s:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

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ä	Aay79072	Adj80338	Aau02544	Aay96060	Aau02558	Aau02612	Aau02627	Aau02629	Aaw19883	Aau02542	Aau02551	Aau02585	Adk17416	Adg42838	Abm85072	Abm85084	Abp45887	Adg96714	Abp46044	Adg96871	Adg34301	Adg34317	Abp45916	Adg96743	Adg34310
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9	AAY79072	ADJ80338	AAU02544	AAY96060	AAU02558	AAU02612	AAU02627	AAU02629	AAW19883	AAU02542	AAU02551	AAU02585	ADK17416	ADG42838	ABM85072	ABM85084	ABP45887	ADG96714	ABP46044	ADG96871	ADG34301	ADG34317	ABP45916	ADG96743	ADG34310
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% Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
Score	35	35	35	35	35	35	35	35	35	35	35	35	35	35	35	35	35	35	35	35	35	35	35	35	35
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ADG34306 ADG34303 ADG34303 ADG34303 ADG96742 ADG98057 ADG34308 ADG34308 ADG34308 ADG96723	ABP45923 ABP45923 ABP45917 ABP45696 ABP45888
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## ALIGNMENTS

Complementarity determining region 2; CDR2; antibody; Gla domain; factor IX/IXa; blood coagulation; deep venous thrombosis; light chain; arterial thrombosis; unstable angina; post myocardial infarction; coronary artery bypass graft; CABG; stroke; tumour growth; metastasis; percutaneous transluminal coronary angioplasty; PTCA; inflammation; septic shock; hypotension; adult respiratory distress syndrome; ARDS; arterial fibrillation; disseminated intravascular coagulopathy; DIC. Anti-factor IX/IXa antibody L chain V domain CDR2 amino acid sequence AAY79072 standard; peptide; 7 AA. 12-JUN-2000 (first entry) AAY79072; 

Homo sapiens.

WO200012562-A1.

09-MAR-2000.

99WO-US019453. 26-AUG-1999; 98US-0098233P. 99US-0122767P. 28-AUG-1998; 03-MAR-1999;

(GETH ) GENENTECH INC.

Adams CW, Devaux B, Eaton DL, Hass PE, Judice JK, Kirchhofer D; Suggett  $S_{\it i}$ 

WPI; 2000-256595/22.

Novel human anti-Factor IX/IXa antibodies against IX/IXa gamma-carboxyglutamic acid domains useful as anti-coagulant in thrombosis, stroke, and post myocardial infarction.

Claim 8; Fig 2; 84pp; English.

This sequence represents a complementarity determining region 2 (CDR2) of the light chain variable domain of a human anti-factor IX/IXa Gla domain antibody. Factor IXa is a vitamin K dependent plasma serine protease that participates in the blood coagulation pathways. The Gla domain of factor IXa and its zymogen factor IX contains important structural determinants for interaction with high affinity binding sites on vascular endothelial

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The invention relates to a method of producing a hybrid antibody or hybrid antibody fragment by: (1) providing an initial antibody having epcificity for a traget; (1) determining the sequence of a variable region of the initial antibody; (11) selecting a first component of the region consisting of FR1, FR2, FR3 and FR4; (1v) comparing the sequence of the first component to sequences contained in a reference database of antibody sequences or antibody fragment sequences from a target species; (v) selecting a sequence from an antibody in the database which demonstrates a high degree of homology to the first component; (vi) selecting a second component of the variable region which is different than the first component, the second component selected from the group consisting of FR1, FR2, FR3 and FR4; (vi) comparing the sequence of the second component to sequences contained in a reference database of antibody sequences or antibody fragment sequences from the target species; (viii) selecting a sequence from the database which demonstrates a high degree of homology to the second component and which is from a different antibody than the selected antibody; and (ix) operatively linking the
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the treatment or prophylaxis of thrombotic or coagulopathic diseases or the treatment or prophylaxis of thrombotic or coagulopathic diseases or disorders in a mammal for which inhibiting a FIX/IX mediated event is indicated, e.g. deep venous thrombosis, arterial thrombosis, unstable angina, post myocardial infarction, post surgical thrombosis, coronary artery bypass graft (CABG), percutaneous transluminal coronary artery bypass graft (throw the transluminal coronary inflammation, septic shock, hypotension, adult respiratory distress syndrome (ARDS), arterial fibrillation and disseminated intravascular coagulopathy (DIC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Producing a hybrid antibody or hybrid antibody fragment by operatively linking the selected framework sequences to one or more complementarity determining regions of the initial antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hybrid antibody; antibody; framework region; homology; immunogenicity.
                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                       Length 7;
                                                                                                                                                                                                                                                                                                                0; Indels
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                                                                                                                                                                                                                                                                       100.0%; Score 35; DB 3; L
100.0%; Pred. No. 1.8e+06;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADJ80338 standard; protein; 99 AA.
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Best Local Similarity 100.000
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                                                                                                                                                                                                                                                                                                                                                                              1 DVSKRPS 7
                                                                                                                                                                                                                                                                                                                                                         1 DVSKRPS
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                                                                                                                                                                                                                               Sequence 7 AA;
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ANU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
and heavy chain complementarity determining regions (CDR) of the
invention. The antibodies can be used in the treatment of obesity and
obesity related diseases. The antibodies can be used to deliver drugs or
pro-drugs directly to the far mass of an obese patient or the antibody
can be used as a therapeutic itself. Antibodies binding specifically to
adipocytes can be used to activate the immune system to destroy the cells
of complement mediated lysis. The antibodies may be labeled with a
detectable label such as radiolabel, fluorescent or chemical group and
used in methods of diagnosis in human subjects e.g. to determine the
presence of adipocyte antigen on the surface of an adipocyte sample.
The antibodies can be used as an alternative means of treatment for obese
the antibodies can be used as an alternative means of treatment for obese
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selected framework sequences to one or more complementarity determining regions (CDRs) of the initial antibody to produce a hybrid antibody or hybrid antibody fragment. The method is useful for producing a hybrid antibody or hybrid antibody fragment (claimed). The antibody and fragments are useful for therapeutic and diagnostic purposes. The method uses entire framework regions from a single antibody variable heavy or variable light chain to receive the CDRs. This produces antibodies that are highly homologous and exhibit reduced immunogenicity while maintaining an optimum binding profile. This sequence represents the amino acid sequence of an antibody from the Vlambda gene locus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Panel of specific binding members of antibody molecules which bind to whole adipocytes is used in the treatment of obesity and obesity related
                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                     100.0%; Score 35; DB 7; Length 99; 100.0%; Pred. No. 5.4;
                                                                                                                                                                                                                                                                                                           0; Indels
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                                                                                                                                                                                                                                                                                                             0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAU02544 standard; protein; 109 AA.
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Best Local Similarity 100.
Matches 7; Conservative
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                                                                                                                                                                                                                                 Sequence 99 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Making antibodies (e.g. anti-decay accelerating factor antibody) for diagnosing or treating e.g. lung cancer comprises identifying an antigen that is differentially expressed on the surface of two or more distinct cell populations.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is that of the light chain variable region (VL) of the anti-decay accelerating factor (DAF) human antibody LU30. The VH region is given in AAY06063. LU30 has a binding affinity (Kd) for DAF of about 13 nM. It was produced using a novel method for making antibodies which can be used for cancer diagnosis or therapy. The method comprises:
                                                                Gaps
for different types of fat deposits can also be produced e.g. intra-
abdominal fat associated with heart disease
                                                                                                                                                                                                                       LU30; human; antibody; VL domain; decay accelerating factor; DAF; chage display; subtractive panning; lung cancer; lung carcinoma; lung adenocarcinoma; therapy; diagnosis.
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/label= CDRIII
/note= "complementarity determining region III"
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                                                                                                                                                                                                                                                                                                                                                        /note= "complementarity determining region II"
                                                                                                                                                                                                                                                                                       23. .36
/label= CDRI
/note= "complementarity determining region
                                             4; Length 109;
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                                                              0, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                       "hypervariable loop residues"
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te= "hypervariable loop residues"
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:e= "hypervariable loop region"
                                           100.0%; Score 35; DB
100.0%; Pred. No. 6;
ive 0; Mismatches
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/label= CDRII
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                                  Query Match
Best Local Similarity luv...
7; Conservative
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                                                                                            DVSKRPS 57
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                          Sequence 109 AA;
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(a) binding an antibody phage from a naive antibody phage library to a live cancer cell; (b) selecting an antibody phage or antibody which binds selectively to the live cancer cell; and (c) identifying an antibody which the antibody phage or antibody binds. To obtain LU30, a human scrvulbrary was used to search for tumour-associated antigens by panning the lung adenocarcinoma cell line 1264, and counter-selecting with a non-tumour bronchial epithelial cell line 188A-2B. The invention also describes a method for identifying an antigen which is differentially expressed on the surface of 2 or more distinct cell populations. The anti-DAF human antibody, or a composition comprising the antibody, is useful for in vivo cancer diagnosis or therapy. In particular, the antibody is useful lor diagnosing or treating lung cancer, e.g. small cell lung cancer, non-small cell lung cancer, large cell lung carcinoma, lung adenocarcinoma, or squamous cell lung carcinoma (all claimed)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Panel of specific binding members of antibody molecules which bind to whole adipocytes is used in the treatment of obesity and obesity related
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Best Local Similarity 100.
Matches 7; Conservative
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N-PSDB; AAS03458.
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and heavy chain complementarity determining regions (CDR) of the and heavy chain complementarity determining regions (CDR) of the invention. The antibodies can be used in the treatment of obesity and obesity related diseases. The antibodies can be used to deliver drugs or pro-drugs directly to the fat mass of an obese patient or the antibody can be used as a therapeutic Itself. Antibodies binding specifically to adipocytes can be used to activate the immune system to destroy the cells by complement mediated lysis. The antibodies may be labeled with a detectable label such as radiolabel, fluorescent or chemical group and cetectable label such as radiolabel, fluorescent or chemical group and cetectable label such as radiolabel, fluorescent or chemical group and cetectable label such as radiolabel, fluorescent or chemical group and cetectable label such as radiolabel, fluorescent or chemical group and cetermine the presence or level of adipocytes in a cell or tissue sample. The antibodies can be used as an alternative means of treatment for obese for different types of fat deposits can also be produced e.g. intra-abdominal fat associated with heart disease
presence of adipocyte antigen on the surface of an adipocyte to detect or determine the presence or level of adipocytes in a cell or tissue sample. The antibodies can be used as an alternative means of treatment for obese patients other than undergoing surgery to remove excess fat. Antibodies for different types of fat deposits can also be produced e.g. intraabdominal fat associated with heart disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Panel of specific binding members of antibody molecules which bind to whole adipocytes is used in the treatment of obesity and obesity related diseases.
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                                                                                                                                                                               100.0%; Score 35; DB 4; Length 110;
100.0%; Pred. No. 6.1;
ive 0; Mismatches 0; Indels
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Matches
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AAU02612
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Sequence 110 AA;

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and heavy chain complementarity determining regions (CDR) of the and heavy chain. Take and heavy chain complementarity determining regions (CDR) of the invention. The antibodies can be used in the treatment of obesity and obesity related diseases. The antibodies can be used to deliver drugs or pro-drugs directly to the fat mass of an obese patient or the antibody can be used as a therapeutic itself. Antibodies binding specifically to adipocytes can be used to activate the immune system to destroy the cells by complement mediated lysis. The antibodies binding specifically to adipocyte and an antibodies may be labeled with a detectable label such as radiolabel, fluorescent or chemical group and used in methods of diagnosis in human subjects e.g. to determine the presence or level of adipocytes in a cell or tissue sample. The antibodies can be used as an alternative means of treatment for obese patients other than undergoing surgery to remove excess fat. Antibodies for abdominal fat associated with heart disease
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 DB 4; Length 110;
                                                                                                                                                                                                                                                                                                                       Antibody; adipocyte; heavy chain; light chain; obesity;
heart disease; complementarity determining region; CDR.
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                                 Mismatches
100.0%; Score 35; 100.0%; Pred. No.
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                                                                                                                                                                                      AAU02627 standard; protein; 110 AA
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                                   7; Conservative
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N-PSDB; AAS03527.
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Query Match
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AAU02629;

RESULT 8

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This polypeptide sequence comprises the light chain variable region (VL) of human carcinoembryonic antigen (hCEA) specific antibodies CEA1, CEA2 and CEAA. WH (AAT72123-35) gene sequences were obtained for anti-hCEA antibodies CEA1-CEA7 (see AAM19876-85). A claimed specific binding member (A) comprises an hCEA specific antibody antigen binding domain that has a dissociation constant for hCEA of less than 1 x 10 -8 M, is non-cross-reactive with human liver cells, and preferentially binds to the A1-B3 extracellular domain of hCEA and/or to cell-associated hCEA over hCEA over soluble hCEA. Preferred (A) include pairings of VH and VL sequences from CEA1-7, or their CDR sequences, as well as CEA6 VH and VL variants. (A) is used to detect cells expressing hCEA, in vivo or in vitro, especially tumour cells for diagnosing cancer, e.g. adenocarcinoma of the colon, lung or breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Specific binding members for human carcinoembryonic antigen - bind to the A3-B3 extracellular domain of hCEA and are substantially non-cross-reactive with human liver cells; used for diagnosing cancer.
                                                                                      Carcinoembryonic antigen; CEA; human; antibody; scFv; tumour marker; lung cancer; breast cancer; colon cancer; adenocarcinoma; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                               /label= CDR3
/note= "complementarity determining region 3"
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90. .100
                                                                                                                                                                                                                                                                    "complementarity determining region 1"
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                                            CEA-specific antibody CEA1, CEA2, CEA3 VL sequence.
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/label= CDR2
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/label= CDR1
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07-DEC-1997 (first entry)
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                                                                                                                                                                                                                                                                           /note=
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N-PSDB; AAT72133.
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23-MAY-1996;
11-OCT-1996;
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sequences of anti-adipocyte monoclonal antibody heavy chain. light chain,
and heavy chain complementarity determining regions (CDR) of the
invention. The antibodies can be used in the treatment of obesity and
conserved as a conserved of the far mass of an obese patient or the antibody
can be used as a therapeutic itself. Antibodies binding specifically to
adipocytes can be used to activate the immune system to destroy the cells
by complement mediated lysis. The antibodies binding specifically to
adipocytes can be used to activate the immune system to destroy the cells
by complement mediated lysis. The antibodies binding specifically to
can be used as a therapeutic itself. Antibodies binding specifically to
detectable label such as radiolabel, fluorescent or chemical group and
cused in methods of diagnosis in human subjects e.g. to determine the
consequence of adipocyte antigen on the surface of an adipocyte to detect or
determine the presence or level of adipocytes in a cell or tissue sample.
The antibodies can be used as an alternative means of treatment for obese
consequence of adipocyte of fat deposits can also be produced e.g. intra-
abdominal fat associated with heart disease
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                                                                                                                                                                                                                       Anti-adipocyte monoclonal antibody light chain, FAT 113.
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                                                                                      AAU02629 standard; protein; 110 AA.
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DVSKRPS 57
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tes 7; Conserv
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AAW19883

AAW19883 ID AAW1 XX AC AAW1 XX

RESULT 9

Query Match

Matches

AAU02542;

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sequences of anti-adipocyte monoclonal antibody heavy chain, light chain, and heavy chain complementarity determining regions (CDR) of the invertion. The antibodies can be used in the treatment of obesity and obesity related diseases. The antibodies can be used to deliver drugs or pro-drugs directly to the fat mass of an obese patient or the antibody and be used as a therapeutic itself. Antibodies binding specifically to adipocytes can be used to activate the immune system to destroy the cells by complement mediated lysis. The antibodies may be labeled with a detectable label such as radiolabel, fluorescent or changel and
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100.0%; Pred. No. 6.1;
tive 0; Mismatches 0; Indels
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N-PSDB; AAS03451.
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52 DVSKRPS
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Homo sapiens.
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AAU02585
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Panel of specific binding members of antibody molecules which bind to whole adipocytes is used in the treatment of obesity and obesity related
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                                                                                                               Antibody; adipocyte; heavy chain; light chain; obesity; fat; heart disease; complementarity determining region; CDR.
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100.0%; Score 35; DB 4; Length 111;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 7; Conservative 0; Mismatches 0. Trans
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                                                                    Anti-adipocyte monoclonal antibody light chain, FAT 30.
                                                                                                                                                                                                                                                                                                                                                                                                                                    (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 118-119; 182pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU02551 standard; protein; 111 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Vaughan TJ;
                                                                                                                                                                                                                                                                                                                                                                                       99US-0158812P
                                                                                                                                                                                                                                                                                                                                       11-OCT-2000; 2000WO-GB003900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                    29-AUG-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Main SH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-282031/29.
N-PSDB; AAS03442.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51 DVSKRPS 57
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                                                                                                                                                                                                                                           WO200127279-A1.
                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                       12-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Edwards BM,
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diseases.

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Gaps

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fat;

AAU02551;

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WPI; 2003-731501/69.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADG42838;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (PAUL/)
(ZHUL/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HUAS/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hua S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADG42838
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                      AAU02501-AAV02635, and AAU02641-AAU02748 represent the amino acid
sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
and heavy chain complementarity determining regions (CDR) of the
invention. The antibodies can be used in the treatment of obseity and
chugs directly to the fat mass of an obses patient or the antibody
can be used as a therapeutic itself. Antibodies binding specifically to
an be used as a therapeutic itself. Antibodies binding specifically to
adipocytes can be used to activate the immune system to destroy the cells
by complement mediated lysis. The antibodies may be labeled with a
detectable label such as radiolabel, fluorescent or chemical group and
used in methods of diagnosis in human subjects e.g. to determine the
presence of adipocytes antigen on the surface of an adipocyte to detect or
determine the presence or level of adipocytes in a cell or tissue sample.
The antibodies can be used as an alternative means of treatment for obese
for different types of fat deposits can also be produced e.g. intra-
abdominal fat associated with heart disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                Panel of specific binding members of antibody molecules which bind to whole adipocytes is used in the treatment of obesity and obesity related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          anti-HIV; cytostatic; virucide; single chain antibody; antibody; yeast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 35; DB 4; Length 111; 100.0%; Pred. No. 6.1; cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Anti-human CXCR4 loop 6 ScFv antibody Vl region.
                         (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADK17416 standard; protein; 111 AA.
                                                  Vaughan TJ;
                                                                                                                                                                  Claim 1; Page 146; 182pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-FEB-2002; 2002US-00071866.
08-FEB-2002; 2002US-00072031.
25-APR-2002; 2002US-00133978.
99US-0158812P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-FEB-2003; 2003WO-US003763.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zhu L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GENE-) GENETASTIX CORP.
                                                  Main SH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pauling MH,
                                                                           WPI; 2001-282031/29.
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DVSKRPS 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 DVSKRPS 7
                                                                                         N-PSDB; AAS03485
                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 111 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO2003066830-A2.
12-0CT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HIV; cancer;
                                                  Edwards BM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-AUG-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADK17416;
                                                                                                                                           diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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Matches
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The invention relates to a method of selecting a single chain antibody (scFv) against a peptide target in a yeast by expressing a library of scFv) against a peptide target in a yeast by expressing a library of scFv fusion proteins in yeast cells expressing the scFv fusion proteins brotein protein.

In the yeast cells expressing the scFv fusion proteins baving either the DNA binding domain or the activation domain of the transcription cartivator which is not comprised in the scFv fusion proteins, and a ctrarget peptide, and selecting those yeast cells in which a reporter gene is expressed. Each scFv fusion protein comprises either an activation domain or a DNA binding domain of a transcription activator and a scFv having a heavy chain of a variable region (WI) of antibody whose sequence varies within the library, a light chain of a variable region (WI) of antibody whose sequence varies within the library independently of the Cr antibody whose sequence varies within the library independently of the Cr corned by binding of the scFv fusion protein to the target fusion creporter gene is activated by a reconstituted transcriptional activator formed by binding of the scFv fusion protein to the target fusion creporter. The methods and compositions of the protein. The methods and compositions of the proventing and/or treating HIV infection and cancer. This sequence corresponds to the VI region of an anti-human CXCR4 loop 6 antibody gene corresponds to the VI region of an anti-human cXCR4 loop 6 antibody gene corresponds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
Selecting an scFv against a peptide target by expressing a target fusion procein having a DNA binding domain or activation domain of a transcription activator, useful for diagnosing, preventing and/or treating HIV infection and cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HIV infection; HIV type 1; HIV type 2; cancer; breast; prostate; liver; renal; lung; skin; ovarian; cervical; brain; thyroid; stomach; colon; lymphoma; leukaemia; pancreas; chemokine receptor; antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 35; DB 7; Length 111; 100.0%; Pred. No. 6.1; cive 0; Mismatches 0; Indels
                                                                                                                                              Claim 123; SEQ ID NO 61; 150pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        scFv Ab124 light chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADG42838 standard; protein; 111 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-FEB-2002; 2002US-00071866.
08-FEB-2002; 2002US-00072301.
25-APR-2002; 2002US-00133978.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-FEB-2003; 2003US-00360828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pauling MH, Zhu L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-FEB-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity luv...
7; Conservative
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PAULING M H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2004-051479/05
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 111 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US2003206909-A1
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                                                                                                      The invention relates to an antibody that binds to loop 6 of human chemokine receptor (CKCR4). The antibody is useful in the treatment or prevention of HIV infection (e.g. HIV type 1 and HIV type 2) and cancer of (e.g. breast, prostate, liver, renal, lung, skin, ovarian, cervical, brain, thyroid, stomach, colon, lymphoma, leukaemia and pancreas cancer cells), for screening furgs, for diagnosing disease or condition associated with interaction with chemokine receptor. The present sequence is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to novel diagnostic and therapeutic polynucleotides selected from one of the 2722 sequences defined in the specification. A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gietzen D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New diagnostic and therapeutic polynucleotides and polypeptides, useful in diagnosing a condition, disease or disorder associated with human molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or in gene mapping.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
Harthshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;
Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;
Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;
Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;
Ru Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietze
Patury S, Shi X, Suarez CJ;
                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
                             Antibody binding loop of human chemokine receptor useful for the treatment of HIV infection and cancer.
                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                              100.0%; Score 35; DB 8; Length 111; 100.0%; Pred. No. 6.1;
                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human diagnostic and therapeutic pprotein SEQ ID NO:5321.
                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                          Claim 6; SEQ ID NO 61; 74pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABM85072 standard; protein; 214 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 27; Page; 190pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-SEP-2003; 2003WO-US028227.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-SEP-2002; 2002US-0410259P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-NOV-2004 (first entry)
                                                                                                                                                                                                                                                                                                                7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2004-329368/30
                                                                                                                                                                                                                                                                                                                                                                            DVSKRPS 58
                                                                                                                                                                                                                                                                                                                                               1 DVSKRPS 7
                                                                                                                                                                                                                                                                                                Local Similarity
N-PSDB; ADG42836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; ACN43724
                                                                                                                                                                                                                                                   Sequence 111 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO2004023973-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-MAR-2004
                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 15
                                                                                                                                                                                                                                                                                                   Best
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CC diagnostic and therapeutic polymucleotides (dithp) or polypeptides may be disponselt and therapeutic polymucleotides (dithp) or polypeptides may be cu used to diagnoste a particular condition, disease or disorder associated with human molecules, e.g. cell proliferative disorders, autoimmune/inflammancy disorder, developmental disorders, or autoimmune/inflammancy disorder, gastrointestinal disorders, or disorder, neurological disorders, gastrointestinal disorders, or infections caused by virus, bacteria, fungi or parasite. The dithp complecules may also be used in genetic mapping) in identifying individuals complecules may also be used in genetic mapping, in identifying individuals complecules may also be used in detecting single nucleotide constitutes, as molecular weight markers, and for somatic or germline complements as molecular weight markers, and for somatic or germline convention. Note: The sequence fargement is not represented in the printed specification, but was obtained in electronic format directly convention. Note: The sequence of this patent is not represented in the printed specification, but was obtained in electronic format directly care. Multiply match as a conservative or mismatches or indels or independent or indels or inde
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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- protein search, using sw model OM protein October 14, 2005, 16:02:59; Search time 9.73438 Seconds (without alignments) 69.190 Million cell updates/sec Run on:

US-10-614-959-14 35 Title: Perfect score:

1 DVSKRPS 7 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

	Description	Ig lambda chain -		Ig lambda chain V-	type am	Ig lambda chain V-		ody 1		lambda		Ig lambda chain V-	type II site-speci	hypothetical prote	hypothetical prote		homeobox protein M	probable protein p	hypothetical prote	hypothetical prote	probable receptor-	hypothetical prote	υ		hypothetical prote	ADP, ATP carrier pr			e cycloh	Ig lambda chain -
	ΠD	0	G85056	A24626	A38923	L2HUTR	F64690	S51149	L2HUWN	S36281	S31515	S44105	S26836	AH2642	A97425	E70191	A32548	T00750	T21466	T21806	T00850	H84903	T37715	T21800	G84897	T09711	L2HUMC	AE1316	AE1688	825759
	8		~	N	~	Н	7	7	Н	7	~	~	7	7	N		~	~	7	~	N	~	~	N	7	~	Н	~	N	0
	Match Length	66	646	9	103	111	423	110	111	111	112	112	416	74	88	337	377	404	685	069	735	972	1033	1077	1245	91	111	189	189	235
* Query	Match	100.0	97.1	91.4	91.4	91.4	91.4	88.6	88.6	98.6	85.7	85.7	85.7	82.9	82.9	82.9	82.9	82.9	82.9	82.9	82.9	82.9	82.9	82.9	82.9	80.0	。	80.0	80.0	80.0
	Score	m	34	32	32	32	32	31	31	31	30	30	30	29	29	29	29	29	29	29	29	29	29	29	29	28	28	28	28	28
Result	No.	-	~	n	4	ß	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26		28	29

ig lambda chain - 60s ribosomal prot hypothetical prote hypothetical prote hypothetical prote mytants block spor thioredoxin-disult thioredoxin reduct thioredoxin reduct familial Alzheimer SRPMSA protein - hymothetical noree	gene 12 protein - 4-hydroxybutyryl-C pseudolysin (BC 3.
\$14675 T40075 A64624 D71891 A82017 A830243 E830299 B97777 G87604 S65358 S35481	Z2BPC2 F90422 HYBSPA
0000000000000000	1404
233 292 292 390 390 391 391 444 444 667	4.4.4.4.4.9.00.00.00.00.00.00.00.00.00.00.00.00.0
	80.00
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	00000
	4444 5444 5

## ALIGNMENTS

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1g lambda chain - human (fragment)
[g lambda chain - human (fragment)
[c;Species: Homo sapiens (man)
[c;Species: 22-Nov-1993 #sequence_revision 01-Dec-1995 #text_change 21-Jan-2000
[c;Accession: S36057
[c]Accession: S36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Cross-references: EMBL: Z22198; NID: 9312319; PIDN: CAA80208.1; PID: 9312320 C; Superfamily: immunoglobulin V region; immunoglobulin homology C; Keywords: heterotetramer; immunoglobulin F: 15-92/Domain: immunoglobulin homology < IWM>
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Gaps ö Query Match 100.0%; Score 35; DB 2; Length 99; Best Local Similarity 100.0%; Pred. No. 1.1; Matches 7; Conservative 0; Mismatches 0; Indels

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1 DVSKRPS 7 8 a probable receptor-like protein kinase [imported] - Arabidopsis thaliana probable receptor-like protein kinase [imported] - Arabidopsis thaliana (mouse-ear cress)

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: ile-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Aug-2004

C;Accession: GB5056

R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Sprin Asture 402, 769-777, 1999

A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.

A;Reference number: A85001; MUID:20083488; PMID:10617198

A;Accession: GB5056

A;Accession: BF5056

A;Accession: Breliminary

A;Residues: 1-646 <STO>

A;Cross-references: UNIPROT:Q9XEC7; GB:NC_001268; NID:g7267207; PIDN:CAB77918.1; GSPDB:G C;Genetics:

A;Gene: AT4g04500 A;Map position: 4 C;Superfamily: protein kinase homology

Gaps ö Length 646; 0; Indels Query Match 97.1%; Score 34; DB 2; Best Local Similarity 85.7%; Pred. No. 12; Matches 6; Conservative 1; Mismatches

ö

1 DVSKRPS 7

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A.Chrose-references: GDB:119342; OMIM:147240
A.Grose-references: GDB:119342; OMIM:147240
A.Map position: 22q11.2-22q11.2
C.Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kalman disulfide bonds: In some cases, such as IgA and IgM, the subunits associate into la C.Superfamily: immunoglobulin V region; immunoglobulin homology
C.Keywords: blocked amino end; heterotetramer; immunoglobulin
F:15-92/Domain: immunoglobulin homology <IMM>
F:16-92/Domain: immunoglobulin homology <IMM>
F:17-93/Domain: and (GIN) (probably pyrrolidone carboxylic acid) #statup F:22-90/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       type IIS restriction enzyme R protein - Helicobacter pylori (strain 26695)
C;Species: Helicobacter pylori
C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
C;Accession: F64690
R;Pomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D. Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.A.; Khalak, H.G.; Glodek, A.; McKenncson, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L. Nature 388, 539-547, 1997
A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.A;Reference number: A64520; MUID:97394467; PMID:9252185
A;Accession: F64690
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C;Speciés: Homo sapiens (man)
C;Date: O'T-May-1995 #sequence_revision 01-Sep-1995 #text_change 21-Jan-2000
C;Accession: S51149
R;de Kruif, J.; Boel, E.; Logtenberg, T.
R;de Kruif, J.; Boel, E.; Logtenberg, T.
A;Description: Selection and application of human SCFV antibody fragments from a semi-sy A;Reference number: S51147
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                                                                                                                                                                                                                                                                                                                        91.4%; Score 32; DB 1; Length 111; 85.7%; Pred. No. 5.9; tive 1; Mismatches 0; Indels
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Pred. No. 23;
1; Mismatches 0; Indels
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A;Residues: 1-110 <-DEK>
A;Cross-references: BMBL:X83712
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;13-90/Domain: immunoglobulin homology <-IMM>
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85.7%; Pred. No. 9.8;
iive 1; Mismatches
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85.7%;
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Best Local Similarity 85.7
Matches 6; Conservative
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52 DVTKRPS 58
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Best Local Similarity
Matches 6; Conserv
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Best Local Similarity
Matches 6; Conserr
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A; Status: preliminary
A; Molecule type: mRNA
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R; Bulitz, M.; Linke, R.P.
Biochem. Biophys. Res. Commun. 194, 1427-1434, 1993
B; Cillie: The precursor molecule of a V-lambda II-immunoglobulin light chain-derived amyl A; Reference number: A38923; MUD:99356823; PMID:8352801
A; Reference number: A38923; MUD:99356823; PMID:8352801
A; Accession: A38923
A; Molecule type: protein
A; Residues: 1-95;96-103 cEUL>
A; Residues: 1-95;96-103 cEUL>
C; Comment: This protein is derived from an immunoglobulin light chain of lambda type. C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: amyloid; immunoglobulin
F:1-58/Product: AL type amyloid fibril protein #status predicted cMAT>
F;7-83/Domain: immunoglobulin homology cIMM>
                                                                                                                                                                                                                                                   Circustion A24626
Ribultz, M.; Linke, R.
Balol. Chem. Hoppe-Seyler 366, 907-915, 1985
Balol. Chem. Hoppe-Seyler 366, 907-915, 1985
A;Title: Amyloid fibrils derived from V-region together with C-region fragments from a A;Reference number: A24626; MUID:86077295; PMID:3935132
A;Accession: A24626
A;Accession: A24626
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
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(Species: Homo sapiens (man)

(Species: Homo sapiens (man)

(Spacies: Homo sapiens (man)

(Spacies: 29-Jul-1981 #sequence_revision 29-Jul-1981 #text_change 09-Jul-2004

(SAccession: A01973

Rischolz, R.; Yang, C.; Hilschmann, N.

Hoppe-Seyler's Z. Physiol. Chem. 360, 1903-1918, 1979

A; Title: Zur Strukturregel der Antikoerper. Die Primaerstruktur eines monoklonalen IgA 3Accession: A01973

A; McCession: A01973

A; McSeidues: Loctein

A; Residues: 1-11 - «SCH»

A; Residues: 1-11 - «SCH»

A; Residues: 1-11 - «SCH»
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                                                                                                                                                             Ig lambda chain V-II region (Har) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 25-Oct-1987 #sequence_revision 25-Oct-1987 #text_change 16-Aug-1996
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Pred. No. 3.1;
1; Mismatches 0; Indels
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C;Comment: This chain was isolated from a myeloma protein.
C;Genetics:
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Best Local Similarity 85.7%;
Matches 6; Conservative
         DISKRPS 612
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submitted to the EMBL Data Library, January 1993
A;Description: V-lambda-2 gene sequence of a high affinity anti-idiotypic IgM antibody f
A;Reference number: S31515
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: 344105
R;Hawkins, R.E.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.
submitted to the EMBL Data Library, March 1994
A;Abeaription: Idiorypic vaccination against human B-cell lymphoma: rescue of variable r
A;Accession: §44105
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*Residues 1-416 < CBC>
A;Cross-references: UNIPROT:P23191; EMBL:X56977; NID:g44180; PIDN:CAA40298.1; PID:g44182
C;Keywords: hydrolase
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R'BockLage, H.; Heeger, K.; Mueller-Hill, B.
R'BockLage, H.; Heeger, K.; Mueller-Hill, B.
Nucleic Acids Res. 19, 1007-1013, 1991
Aritle: Cloning and characterization of the MboII restriction-modification system.
A; Reference number: S26835; MUID:91212177; PMID:2020540
A; Accession: S26835
A; Status: Preliminary
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C.Date: 03-Mar-1994 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
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Cs:Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-92/Domain: immunoglobulin homology <IMM>
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A; Status: preliminary
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-112 <VAN>
A; Residues: DNA
C; Superferances: EMBL: 219546; NID: 933754; PIDN: CAA79606.1; PID: 933755
C; Superferantly: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F;15-92/Domain: immunoglobulin homology <IVM>
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Pred. No. 17;
0; Mismatches
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Pred. No. 17;
0; Mismatches
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Ig lambda chain V-J region - human
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Similarity 85.7%;
6; Conservative (
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Similarity 85.7%;
6; Conservative
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Best Local Similarity
Matches 6; Conserv
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Best Local Similarity
Matches 6; Conserv
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A;Molecule type: DNA
A;Residues: 1-112 <HAW>
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Best Local Similarity
Matches 5; Conserv
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                                                                                                                                             Ligitations carain v-ii region (WII) - numan (Tencative Bequence)

C;Species: Homos appiens (man)
C;Date: 30-Nov-1979 #sequence_revision 30-Nov-1979 #text_change 09-Jul-2004
C;Accession: A01978
R;Chan, B.L.; Chiu, Y.Y.H.; Humphrey, R.L.; Poljak, R.J.
Biochim. Biophys. Acta 537, 9-21, 1978
A;Title: Amino acid sequence of the human myeloma lambda chain Win.
A;Reference number: A01978; MUID:79062503; PMID:102365
A;Accession: A01978
A;Molecule type: procein
A;References: UNIPROF:P01712
C;Comment: This is a Bence Jones protein.
C;Generics:
A;Cross-references: UNIPROF:P01712
C;Comment: This is a Bence Jones protein.
C;Generics:
A;Cross-references: GDB:119342; OMIM:147240
A;Cross-references: GDB:119342; OMIM:147240
A;Cross-references: GDB:119342; OMIM:147240
A;Cross-references: GDB:110342; OMIM:147240
A;Map postition: 22q11.2-22q11.2
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds: In some cases, such as IgA and IgM, the subunits associate into la C;Superfamily: immunoglobulin heterotetramer
C;Superfamily: immunoglobulin heterotetramer
F;15-92/Domain: immunoglobulin heterotetram
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 9
836281
Ig lambda chain V region (clone alpha-FOGI-A3) - human (fragment)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Species: O3-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000
C; Jaccession: S36281
R; Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.
EMBO J. 12, 725-734, 1993
A; Title: Human anti-self antibodies with high specificity from phage display libraries.
A; Reference number: S36286, MUID:93178448; PMID:7679990
A; Accession: S36281
A; Status: preliminary; nucleic acid sequence not shown
A; Molecule type: mRNA
A; Residues: 1-111 -GRIS
A; Cross references: EMBL:218823; NID:g33414; PIDN:CAA79275.1; PID:g939907
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F;15-92/Domain: immunoglobulin homology <INM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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831515
Ciplanbda chain V region - human (fragment)
CiSpecies: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
C;Accession: S31515
R;van der Heijden, R.W.J.; Uytdehaag, F.G.C.M.; Osterhaus, A.D.M.E.
                                                                                                                            Ig lambda chain V-II region (Win) - human (tentative sequence)
C;Species: Homo sapiens (man)
C;Date: 30-Nov-1979 #sequence_revision 30-Nov-1979 #text_change 09-Jul-2004
C;Accession: A01978
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85.7%; Pred. No. 9.9;
iive 1; Mismatches 0; Indels
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Best Local Similarity 85.7
Matches 6; Conservative
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Matches 6; Conservative
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52 DVDKRPS 58
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Gaps

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Length 337 0; Indels

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Nature 390, 580-586, 1997
A;Authors: Smith, H.O.; Venter, J.C.
A;Authors: Smith, H.O.; Venter, J.C.
A;Fitle: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
A;Reference number: A70100; MUID:98065943; PMID:9403685
A;Accession: E70191
A;Accession: E70191
A;Accession: E70191
A;Molecule type: DNA
A;Residues: 1-337 <KLB>
A;Residues: 1-337 <KLB>
A;Residues: UNB: A;Residues: UNB: A;Residues: UNB: GB:AE001173; GB:AE000783; NID:g2688665; PIDN:AAC6708
A;Experimental source: strain B31
C;Superfamily: translation factor, SUA5 type
                                                                                                                                                                                                                                                                                                                                                                                              Query Match 82.9%; Score 29; DB 1;
Best Local Similarity 71.4%; Pred. No. 88;
Matches 5; Conservative 2; Mismatches
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141 NISKRPS 147
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A,Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A,Reference number: AB2577; MUD:21608550; PMID:11743193
A,Accession: AH3642
A,Accession: AF642
A,Molecule type: DNA
A,Molecule type: DNA
A,Residues: 1-74 «KUR»
A,Festimental source: strain C58 (Dupont)
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Vugt,
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A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum A;Reference number: A97359; MUID:21608551; PMID:11743194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPROT:Q8UHW8; GB:AE007869; PIDN:AAK86354.1; PID:g15155478; GSPDB:G;Genetics:
C;Genetics:
A;Gene: AGR C 956
A;Map position: circular chromosome
                                                                                                                                                                                                                                 CjAccession: AH2642
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein AGR_C 956 [imported] - Agrobacterium tumefaciens (strain C58, Cered
C;Species: Agrobacterium tumefaciens
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
                                                                                                                                        hypothetical protein Atu0540 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
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R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; Whi son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vug; Bowman, C.; Garland, S.; Pujli, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.
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C;Species: Borrelia burgdorferi (Lyme disease spirochete)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
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Pred. No. 19;
1; Mismatches 1; Indels
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A,Gene: Atu0540
A,Map position: circular chromosome
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Best Local Similarity 71.4%;
Matches 5; Conservative
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Best Local Similarity 71.43
Matches 5; Conservative
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2 DISKEPS 8
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A;Molecule type: DNA
A;Residues: 1-88 <KUR>
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Q6ADP4 Q6LWQ4 Q6LWQ4 Q6SX99 Q9VN46 Q6YEY3 Q6UKW8 Q6LKO5

methanococc drosophila drosophila photobacter agrobacteri erwinia car

646 AA

PRT;

ALIGNMENTS

vitis vinif agrobacteri

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01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
05-NUD-2004 (TrEMBLrel. 27, Last annotation update)
05-NUD-2004 (TrEMBLrel. 27, Last annotation update)
Putative receptor-11ke protein kinase.
Name=T26N6.11; Synonyms=AT4904500;
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; rosids; eurosids II; Erassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BU Arabidopsis sequencing project;

Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.

Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.

- - SIMILARITY: Belongs to the Ser/Thr protein kinase family.

EMBL; AF076243; AAD297621; - .

R EMBL; AL161500; CAB77918.1; - .

R PISP; PG6239; JGCK.

GO; GO:0005524; F:ATP binding; IEA.

GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.

GO; GO:0004674; F:protein smino acid phosphorylation; IEA.

R GO; GO:000468; P:protein smino acid phosphorylation; IEA.

R InterPro; IPR001009; Kinase like.

InterPro; IPR001009; Kinase like.

InterPro; IPR001009; Kinase.

InterPro; IPR00607; Sor_thr kinase.

InterPro; DUF0657; DUF26; Z.

R Pfam; PF00669; Pkinase: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Zhong J., Ma P., Parnell L.D., Chen C.N., Chen B.Y., Mewes H.W., Lemcke K., Mayer K.P.X.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ProDom; PD00001; Prot kinase; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS00101; PROTEIN KINASE DOM; 1.
PROSITE; PS00108; PROTEIN KINASE ST; 1.
ATP-binding; Kinase; Receptor; Serine/threonine-protein kinase;
                                                                                                                                                                                                                                                                                                                                                        Zhong J., Ma P., Parnell L.D., Chen C.-N., Chen E.Y.;
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases
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NCBI_TaxID=3702;
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 O9XEC7
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homo sapien
helicobacte
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                                                                  October 14, 2005, 15:51:44; Search time 46.5938 Seconds (without alignments) 76.932 Million cell updates/sec
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Q6phc0 1
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075e06
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0607a3
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         GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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Q6PJA3
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LV2D HUMAN
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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1: uniprot_sprot:*
2: uniprot_trembl:*
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length: 2000000000
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                                                                                                                              1 DVSKRPS 7
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Match
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E1200574D5864207 CRC64;

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71 DVNKRPS 77
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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       DB 2; Length 646;
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                      0; Indels
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                                                                                                                                                                                                                                                                                                                                                                              11561 MW; 99DC457A12E8F6E1 CRC64;
                                                                                                                                                                                                                                                                                                               SMART; SM0406, 1Gv; 1.
PROSITE; PS50835; IG_LIKE; 1.
Direct protein sequencing; Immunoglobulin V region;
Pyrrolidone carboxylic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                         21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
25-JUL-2004 (Rel. 44, Last annotation update)
Ig lambda chain V-II region FRO.
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                                                                                           111 AA
                      1; Mismatches
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1; Mismatches
              69
      Score 34;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                             91.4%; Score 32;
                                                                                                                                                                                                                                                                 GO, GO:0005576; C:extracellular; NAS. GO; GO:0003823; F:antigen binding; NAS. GO; GO:0008925; F:immune response; NAS. InterPro; IPR007110; Ig-like. InterPro; IPR003596; Ig-v. Pf00047; ig; 1.
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05-JUL-2004 (TrEMBLrel. 27, C;
05-JUL-2004 (TrEMBLrel. 27, L;
05-JUL-2004 (TrEMBLrel. 27, L;
Hypothetical protein.
Homo sapiens (Human).
      97.1%;
85.7%;
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             Best Local Similarity 85.7
Matches 6, Conservative
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Matches 6, Conservative
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606 DISKRPS 612
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                                                                                                                                                                                                                                                                                                                                                                              111 AA;
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                                    1 DVSKRPS 7
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SEQUENCE FROM N.A.
                                                                                                                                                                NCBI_TaxID=9606;
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                                                                                           LV2D HUMAN
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SEQUENCE
       Query Match
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LV2D_HUMAN
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Q6PIQ7
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SEQUENCE FROM N.A.
STRAIN-26695 / ATCC 700392;
MEDILINE-9794467; PubMed-9252185; DOI=10.1038/41483;
Tomb J.-P., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,
Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S.K.,
Dougherty B.A., Nelson K.E., Quackepush J., Zhou L., Kirkness E.F.,
Peterson S.N., Loftus B.J., Richardson D.L., Dodson R.J., Khalak H.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Helicobacter pylori (Campylobacter pylori).
Bacteria, Proteobacteria, Epsilonproteobacteria, Campylobacterales;
Helicobacteraceae, Helicobacter.
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
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Pred. No. 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                   Strausberg R.;
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC030983; AAH30983.1; -.
HSSP; P01709; 1A8J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein.
SEQUENCE 236 AA; 25021 MW; 4A07BEF60A5FD465 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JNN-1998 (TrEMBLrel. 05, Created)
01-JNN-1998 (TrEMBLrel. 05, Last sequence update)
01-JNN-1994 (TrEMBLrel. 05, Last annotation update)
Type IIS restriction enzyme R protein (MBOIIR)
OrderedLocusNames=HP1366;
                                                                                                                                                                                                                                                                                                                                  and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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130 AA

PRT;

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PRELIMINARY;
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                                                                                                                                                                                                                                                                          STRAIN=W83;
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    Q7MUS6
ID Q7MUS6
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Chen B.L., Chiu Y.-Y.H., Humphrey R.L., Poljak R.J.;
Chen B.L., Chiu Y.-Y.H., Humphrey R.L., Poljak R.J.;
Thamino acid sequence of the human myeloma lambda chain Win.";
Biochim. Biophys. Acts 337:9-21(1978).
C.-!- MISCELLANEOUS: This is a Bence-Jones protein.
FIR; A01978; L2HUWN.
RISP; PO1709; 1DCL.
ROJ GO:0005576; C:extracellular; NAS.
ROJ GO:0005576; P:immune response; NAS.
ROJ GO:00059576; P:immune response; NAS.
RICHEPPO; IPR007110; Ig-like.
RICHEPPO; IPR003596; Ig-V.
REPROMATION RE
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Glodek A., McKenney K., FitzGerald L.M., Lee N., Adams M.D., Hickey E.K., Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M., Cotton M.D., Weldman J.F., Fujii C., Bowman C., Walthey L., Wallin E., Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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0
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21-JUL-1986 (Rel. 01, Last sequence update)
21-JUL-2004 (Rel. 44, Last annotation update)
19 lambda chain V-II region WIN.
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                                                                                                                pylori.";
Nature 388:539-547(1997).
EMBL; AE000637; AAD08410.1; -
PIR; F64690; F64690.
                                                                                                                                                                                                    InterPro; IPR003615; HNH_nuc.
SMART; SM00507; HNHC; 1.
Complete proteome.
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71 DMSKRPS 77
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52 DVDKRPS 58
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Best Local Similarity
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Matches 6; Conserv
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ID _LV2I_HUMAN
AC P01712;
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Calagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D., Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B., Baffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B., Biltins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M., Qui D., Ianakiev P., Pedersen D., Nelson M., Washburne M., Selitrennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U., Rothe G.O., Jedd G., Mewes W., Staben C., Marcotte B., Greenberg D., Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gherre S., Kamal M., Kamvysselis M., Mauceli E., Bielke C., Rudd S., Frishman D., Krystofova S., Rasmussen C., Metzenberg R.L., Perkins D.D., Kroken S., Arystofova S., Rasmusen C., Metzenberg R.L., Perkins D.D., Kroken S., Cogoni C., Macino G., Catcheside D., Li W., Pratt R.J., Osmani S.A., DeSouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R., Yarden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R., Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitzg M., Paulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B., The Genome Sequence of the Filamentous Fungus Neurospora crassa.",
                                                                                                                                                                                                                                                                                                                                                    DOI=10.1128/JB.185.18.5591-5601.2003,
Nelson K.E., Fleischmann R.D., DeBoy R.T., Paulsen I.T., Fouts D.E.,
Eisen J.A., Daugherty S.C., Dodon R.J., Durkin A.S., Gwinn M.L.,
Haft D.H., Kolonay J.F., Nelson W.C., Mason T.M., Tallon L., Gray J.,
Granger D., Tettelin H., Dong H., Galvin J.L., Duncan M.J.,
Dewhirst F.E., Fraser C.M.;
"Complete genome sequence of the oral pathogenic bacterium
Porphyromonas gingivalis strain W83.";
J. Bacteriol. 185:5591-5601(2003).
TIGR; PG1409;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -i- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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Eukaryota, Fungi, Ascomycota, Pezizomycotina, Sordariomycetes,
Sordariomycetidae, Sordariales, Sordariaceae, Neurospora.
                                                                                                                                Porphyromonas gingivalis (Bacteroides gingivalis).
Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88.6%; Score 31; DB 2; Length 130; 71.4%; Pred. No. 63; cive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Complete proteome; Hypothetical protein.
SEQUENCE 130 AA; 14455 MW; 3F2E1F64F23E5805 CRC64;
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Last sequence update)
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  Created)
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                                                                                                                                                                                                                                                                                                                                MEDLINE=22829867; PubMed=12949112;
                                                                                                                                                                                      Porphyromonadaceae; Porphyromonas.
NCBI_TaxID=837;
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01-MAR-2004 (TrEMBLrel. 26, 01-MAR-2004 (TrEMBLrel. 26, 01-MAR-2004 (TrEMBLrel. 26, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                         OrderedLocusNames=PG1409;
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107 DISRRPS 113
                                                                                Hypothetical protein
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STRAIN-YCH46;
Kuwahara T., Yamashita A., Hirakawa H., Nakayama H., Toh H., Okada N.,
Kuhara S., Hattori M., Hayashi T., Ohnishi Y.;
"Genomic analysis of Bacteroides fragilis reveals extensive DNA
inversions regulating cell surface adaptation.";
Proc. Natl. Acad. Sci. U.S.A. 0:0-0(2004).
EMBL; AP006041; BAD48101.1; -.
SEQUENCE 402 AA; 45596 MW; 2D56A6DAF87797CC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C., Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T., Kikuchi H., Shiba T., Sakaki Y., Hattori M.; "Genome sequence of an industrial microorganism Streptomyces avermitilis: deducing the ability of producing secondary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=MA-4680;
MEDLINE=21477403; PubMed=11572948; DOI=10.1073/pnas.211433198;
                                                             Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
Bacteroidaceae; Bacteroides.
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                                                                                                                                                                                                                                                                                                                                                                                                                Length 402;
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InterPro; IPR001128; Cytochrome_P450.
PRINTS; PR00359; BP450.
PROSTIS; PS00086; CYTOCHROME_P450; UNKNOWN 1.
Complete proteome; Heme; Mondoxygenase; Oxidoreductase.
SEQUENCE 486 AA; 53354 MW; A728B74F6592E265 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptomycineae; Streptomycetaceae; Streptomyces.
Predicted nucleoside-diphosphate sugar epimerase
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85.7%; Pred. No. 2.5e+02;
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MEDLINE=22608306; PubMed=12692562;
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Best Local Similarity ا00،،
نام 6; Conservative
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                                           Bacteroides fragilis.
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Best Local Similarity
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                       ORFNames=BF1430;
                                                                                                                        NCBI_TaxID=817
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               EMBL; AABX01000366; EAA30397.1; -. GO; GO:0030288; C:periplasmic space (sensu Gram-negative Bact. . .; IEA. GO; GO:0015035; F:protein disulfide oxidoreductase activity; IEA.
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MEDLINE=22943335; PubMed=14580944; DOI=10.1016/S0306-4522(03)00566-9;
KUCENIAE S., Li Z., Cox J.A., Egan T.M., Voigt M.M.;

"Molecular characterization of the zebrafish P2X receptor subunit gene
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Actinopterygii, Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
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85.7%; Pred. No. 2e+02;
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                                                                                    InterPro; IPR010835; DSBA.
InterPro; IPR010986; DsbA_insertion.
Pfam; PF01323; DSBA; 1.
Hypochetical protein:
SEQUENCE 233 AA; 25367 MW; 50B8F4A369168929 CRC64;
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Last sequence update)
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
ATP-gated ionotropic P2X receptor subunit 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=p2rx2; Synonyms=p2xr2;
Brachydanio rerio (Zebrafish) (Danio rerio).
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Interpro; IPR001429; P2X_receptor.
Pfam; PF00864; P2X_receptor: 1.
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Matches 6; Conservative
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                                                                                                                                                                                                                       PRELIMINARY;
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25-OCT-2004 (
25-OCT-2004 (
25-OCT-2004 (
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RESULT 9 Q64WE5

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AGD; ABL133C;
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Galagan J.B., Calvo S.B., Borkovich K.A., Selker B.U., Read N.D., Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B., Jaffe D., IstzHugh W., Mang S., Nielsen C.B., Butler J., Endrizzi M., Blkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M., Qui D., Ianakiev P., Pedersen D., Nelson M., Washburne M., Schlitch G.P., Kinsey J.A., Braun B.L., Zelter A., Schulte U., Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D., Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S., Ramal M., Kamysselis M., Maucelli E., Bielke C., Rudd S., Frishman D., Krystofova S., Rasmussen C., Metzenberg R.L., Perkins D.D., Kroken S., Cogoni C., Macino G., Catcheside D., Li W., Pratt R.J., Osmani S., Andrew S., Radden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R., Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freiteg M., Paulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B., The Genome Sequence of the Filamentous Fungus Neurospora crassa.";
In Nature 0:0-0(2003).
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PubMed=14665450; DOI=10.1128/EC.2.6.1151-1161.2003;
Catlett N.L., Yoder O.C., Turgeon B.G.;
"Whole-genome analysis of two-component signal transduction genes in
    Gaps
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Cochliobolus heterostrophus (Drechslera maydis).
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;
Pleosporales; Pleosporaceae; Cochliobolus.
                                                                                                                                                                                                                                                                                                                                                               Neurospora crassa.
Bukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
NCBI_TaxID=5141;
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85.7%; Pred. No. 3.8e+02;
iive 0; Mismatches 1; Indels
Indels
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EMBL; AABX01000022; EAA35484.1; -.
SEQUENCE 728 AA; 79550 MW; 05A688EBD3850B79 CRC64;
                                                                                                                                                                                                                                              Created)
Last sequence update)
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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                                                                                                                                                                                                   728 AA
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  1; Mismatches
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  6; Conservative
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Matches 6; Conservative
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                                                                                       428 DVSQRPS 434
                                            1 DVSKRPS 7
                                                                                                                                                                                                                                                                                                                  Predicted protein.
Name=NCU00559.1;
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07SF90
  Matches
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ELEMENTORIC Cell 2:1151-1161(2003).

LINGARTY: Contains 1 histidine kinase domain.

EMBL; AV456014; AAR25980-1; T.

REMBL; AV456014; AAR25980-1; T.

REMBL; AV456014; AAR25980-1; T.

RO; GO:00016202; C:membrane; IEA.

RO; GO:00016202; F:ATP binding; IEA.

RO; GO:0001651; F:LWO-component response regulator activity; IEA.

RO; GO:000155; F:LWO-component signal transduction system (p. .; IEA.

RO; GO:000155; F:LWO-component signal transduction system (p. .; IEA.

RO; GO:000155; F:LWO-component signal transduction system (p. .; IEA.

RO; GO:000155; F:LWO-component signal transduction system (p. .; IEA.

RO; GO:000155; F:LWO-component signal transduction system (p. .; IEA.

RO; GO:000155; F:LWO-component signal transduction system (p. .; IEA.

RO; GO:000155; F:LWO-component signal transduction system (p. .; IEA.

RO; GO:000156; F:LWO-component signal transduction system (p. .; IEA.

RO; GO:000155; F:LWO-component signal transduction system (p. .; IEA.

RO; GO:000156; F:LWO-component signal transduction.

RICEPTO; IRRO0189; Response reg; 1.

REMRT; SM00349; RESPONSE REGULATORY; 1.

ROSITE; PSSO110; RESPONSE REGULATORY; 1.

KWART; SM00349; HIS KIN; 1.

KWART; SM00349; HIS KIN; 1.

ROSITE; PSSO110; RESPONSE REGULATORY; 1.

KWART; ROSITE; PSSO110; RESPONSE REGULATORY; 1.

KWART; ROSITE; PSSO110; RESPONSE REGULATORY; 1.

KWART; ROSITE; ROSIO10; HIS KIN; SMADORY; SERBORY REGULATORY; 1.

KWART; ROSITE; ROSIO10; HIS RIG; REGULATORY; 1.

KWART; ROSITE; ROSIO10; RESPONSE REGULATORY; 1.

KWARTS ROSITE; ROSIO10; RESPONSE REGULATORY; 1.
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Voegeli S.E., Dietrich F.S., Brachat S., Lerch A., Gaffney T.,
Philippsen P.;
Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AE016815; AAS50638.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity 85.7%; Pred. No. 9.6e+02; Similarity 85.7%; Pred. No. 9.6e+02; 6; Conservative 1; Mismatches 0; Indels
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Saccharomycetales; Saccharomycetaceae; Eremothecium,
NCBI TaxID=33169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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ORFNames=ABL133C;
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Poly-Ser.
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                                                          EMBL; AF261918; AAF89106.1; -.
EMBL; AF488803; AAO15765.1; -.
EMBL; AB037733; BAA92550.1; -.
HSSP; P07996; 1LSL.
MEROPS; M12.021; -.
Genew; HGNC:13202; ADAMTS9.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                            A Magase T., Kikuno R., Ishikawa K.T., Hirosawa M., Ohara O.,
A Magase T., Kikuno R., Ishikawa K.T., Hirosawa M., Ohara O.,
A Magase T., Kikuno R., Ishikawa K.T., Hirosawa M., Ohara O.,
The Complete sequences of 150 new cDNA clones from brain which code
T for large proteins in vitro.",
DNA Res. 7:65-73 (2000)

- I- FUNCTION: Cleaves the large aggregating proteoglycans, aggrecan
and versican.

- I- CATALYTIC ACTIVITY: Cleaves aggrecan at the 1838-Glu-|-Ala-1839
site and versican at the 1428-Glu-|-Ala-1429 site.

- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
- SUBGELLULAR LOCATION: Secreted. Associated with the extracellular matrix (By similarity).

- ALTERNATIVE PRODUCTS:

EVENT-ALTERNATIVE PRODUCTS:

EVENT-ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Maki R.A.;
"ADAMTS 9, a novel member of the ADAM-TS/Metallospondin gene family.";
Genomics 67:343-350(2000).
               Also Annual Standard; Fri; 1939 An. O992N4; O99NR29; 16-0CT-2001 (Rel. 40, Created)
16-0CT-2003 (Rel. 45, Last sequence update)
25-0CT-2004 (Rel. 45, Last annotation update)
ADAMTS-9 precursor (EC 3.4.24.-) (A disintegrin and metalloproteinase with thrombospondin motifs 9) (ADAM-TS 9) (ADAM-TS9).
Name-ADAMTS9; Syronyms-KIAA1312; Homo sapiens (Human).
                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORM 1), AND FUNCTION.
MEDLINE=22513925; PubMed=12514189; DOI=10.1074/jbc.M211009200;
SOMETVILLE R.P., Longpre J.-M., Jungers K.A., Engle J.M., Ross M.,
Evanko S., Wight T.N., Leduc R., Apte S.S.;
Evanko S., Wight T.N., Leduc R., Apte S.S.;
Subfamily nelation of Abamys-9 and Abamys-20 as a distinct ADAWTS
subfamily related to Caenorhabditis elegans GON-1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=1; Synonyms=ADAMTS-9B;
IsoId=Q9P2N4-3; Sequence=Displayed;
Name=2; Synonyms=Long;
IsoId=Q9P2N4-1; Sequence=VSP 007548, VSP 007549;
Note=May result from the retention of an intron in the cDNA
                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                         TISSUE=Fetal;
MEDLINE=20396118; PubMed=10936055; DOI=10.1006/geno.2000.6246;
Clark M.E., Kelner G.S., Turbeville L.A., Boyer A., Arden K.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SIMILARITY: Belongs to the peptidase M12B family. -!- SIMILARITY: Contains 1 disintegrin-like domain. -!- SIMILARITY: Contains 1 GON domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SIMILARITY: Contains 15 TSP type-1 domains.
           PRT; 1935 AA
                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 159-1935 FROM N.A. (ISOFORM 2).
                                                                                                                                               SEQUENCE FROM N.A. (ISOFORM 3).
           STANDARD;
                                                                                                                           NCBI_TaxID=9606;
         HUMAN
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InterPro; IPR0018294; ADAM spacer1.

InterPro; IPR001819; Pept M.10A M.12B.

InterPro; IPR001819; Pept M.2B.

InterPro; IPR001890; Peptidase_M12B.

InterPro; IPR001890; Peptidase_M12B.

InterPro; IPR00884; TSP1.

Pfam; PF05866; ADAM spacer1; 1.

Pfam; PF01562; Pep_M12B_propep; 1.

Pfam; PF01562; Pep_M12B_propep; 1.

Pfam; PF00190; TSP1; 1. Zinc (catalytic) (
Zinc (catalytic) (
N-linked (clcnAc.
N-linked (clcnAc. Disintegrin-like Metalloprotease. By similarity. Zinc (catalyti ISP type-1 1. TSP type-1 2
TSP type-1 3
TSP type-1 4
TSP type-1 5
TSP type-1 6
TSP type-1 7
TSP type-1 7
TSP type-1 1

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       monomer (Potential).
SUBUNIT: Oligomer of 24 identical subunits (By similarity).
MISCELLANEOUS: The di-iron binding site functions as active site where iron ions are exidized from iron(II) to iron(III) before they are stored (By similarity).
SIMILARITY: Belongs to the bacterioferritin family.
SIMILARITY: Contains 1 ferritin-like diiron domain.
                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -1- FUNCTION: May perform analogous functions in iron detoxification and storage to that of animal ferritins (By similarity).
-1- COFACTOR: Binds 1 heme b (iron-protoporphyrin IX) group per
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=98072426; PubMed=9409768; DOI=10.1016/S0378-1119(97)00424-1;
                (in isoform 3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Magnetospirillum magnetotacticum (Aquaspirillum magnetotacticum).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales;
Rhodospirillaceae; Magnetospirillum.
       (Potential)
                                                                                                                                                                                                                                                 .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bertani L.E., Huang J.S., Weir B.A., Kirschvink J.L.,
"Evidence for two types of subunits in the bacterioferritin of
Magnetospirillum magnetotacticum.",
Gene 201:31-36(1997).
Score 31; DB 1; Length 1935;
Pred. No. 1.1e+03;
                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Bacterioferritin subunit 1 (BFR 1).
                                                                                                                                                                                                                                                                                                                                                                         164 AA
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InterPro; IPR009078; Perritin/RR like.
InterPro; IPR008331; Ferritin Dps.
InterPro; IPR009040; Ferritin_like.
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PRINTS; PR00601; BACFERRITIN.
                                                                                                                                                                                                                       88.68;
                                                                                                                                                                                                                                                 6; Conservative
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Best Local Similarity
Matches 6; Conserv
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Ferritin-like diiron.
Iron (hew axial ligand) (Potential).
Iron (hew axial ligand) (Potential).
Iron 1 (By similarity).
Iron 2 (By similarity).
Iron 2 (By similarity).
Iron 1 (By similarity).
Iron 2 (By similarity).
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Pred. No. 1.4e+02
1; Mismatches
                                                                                         | Heme; Iron; Iron storage; | Metal-binding. | 147 | Ferritin-like | DOMAIN | 1 147 | Ferritin-like | METAL | 18 18 18 | Iron | (By Sin | METAL | 51 51 | Iron | (By Sin | METAL | 54 54 | Iron | (By Sin | METAL | 54 54 | Iron | (By Sin | METAL | 54 54 | Iron | (By Sin | METAL | 54 54 | Iron | (By Sin | METAL | 54 54 | Iron | (By Sin | METAL | 54 54 | Iron | (By Sin | METAL | 54 54 | Iron | (By Sin | METAL | 54 54 | Iron | (By Sin | METAL | 54 | Iron | (By Sin | METAL | 54 | Iron | (By Sin | METAL | 54 | Iron | (By Sin | METAL | 54 | Iron | (By Sin | METAL | 54 | Iron | (By Sin | METAL | 54 | Iron | (By Sin | METAL | 54 | Iron | (By Sin | METAL | 54 | Iron | (By Sin | METAL | 55 | Iron | (By Sin | METAL | 55 | Iron | (By Sin | METAL | 55 | Iron | (By Sin | METAL | 55 | Iron | (By Sin | METAL | 55 | Iron | (By Sin | METAL | 55 | Iron | (By Sin | METAL | 55 | Iron | (By Sin | METAL | 55 | Iron | (By Sin | METAL | 55 | Iron | (By Sin | METAL | 55 | Iron | (By Sin | METAL | 55 | Iron | (By Sin | METAL | 55 | Iron | (By Sin | METAL | 55 | Iron | (By Sin | METAL | 55 | Iron | (By Sin | METAL | 55 | Iron | (By Sin | METAL | 55 | Iron | (By Sin | METAL | 55 | Iron | (By Sin | METAL | 55 | Iron | (By Sin | METAL | 55 | Iron | (By Sin | METAL | 55 | Iron | (By Sin | METAL | 55 | Iron | (By Sin | METAL | 55 | Iron | (By Sin | METAL | 55 | Iron | (By Sin | METAL | 55 | Iron | (By Sin | METAL | 55 | Iron | (By Sin | METAL | 55 | Iron | (By Sin | METAL | 55 | Iron | (By Sin | METAL | 55 | Iron | (By Sin | METAL | 55 | Iron | (By Sin | METAL | 55 | Iron | (By Sin | METAL | 55 | Iron | (By Sin | METAL | 55 | Iron | (By Sin | METAL | 55 | Iron | (By Sin | METAL | 55 | Iron | (By Sin | METAL | 55 | Iron | (By Sin | METAL | 55 | Iron | (By Sin | METAL | 55 | Iron | (By Sin | METAL | 55 | Iron | (By Sin | METAL | 55 | Iron | (By Sin | METAL | 55 | Iron | (By Sin | METAL | 55 | Iron | (By Sin | METAL | 55 | Iron | (By Sin | METAL | 55 | Iron | (By Sin | METAL | 55 | Iron | (By Sin | METAL | 55 | Iron | (By Sin | METAL | 55 | Iron | (
ProDom; PD002269; Bacterioferritin; 1.
TIGRPAMB; TIGR00754; bfr; 1.
PROSITE; PS00549; BACTERIOFERRITIN; 1.
PROSITE; PS50905; FERRITIN LIKE; 1.
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cch completed: October 14, 2005, 16:19:57 time : 48.5938 secs

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; ORGANISM: Homo sapiens
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Sequence 15, Appl
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                                                                                                   October 14, 2005, 16:00:04; Search time 13.7812 Seconds (without alignments) 37.917 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Description
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.. /cgn2_6/ptodata/1/laa/5A_COMB.pep:*
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.. /cgn2_6/ptodata/1/laa/6A_COMB.pep:*
.. /cgn2_6/ptodata/1/laa/ReCOMB.pep:*
.. /cgn2_6/ptodata/1/laa/ReCOMB.pep:*
.. /cgn2_6/ptodata/1/laa/PcTuS_COMB.pep:*
.. /cgn2_6/ptodata/1/laa/PcTuS_COMB.pep:*
              GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -09-252-991A-23989
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US-08-652-816A-15
US-09-490-070A-19
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US-09-490-153-19
US-09-24-840B-125
US-09-24-840B-125
US-08-487-550-10
US-09-249-016-7859
US-09-38-116-10
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Maximum Match 100%
Listing first 45 summaries
                                                                           - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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Match Length
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Best Local Similarity 100.
Matches 7; Conservative
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COUNTRY: USA
ZIP: 20006
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        New York
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Patent No. 6300064

GENERAL INFORMATION:
APPLICANT: Rnapplik, Achim
APPLICANT: Pack, Peter
APPLICANT: Tlag, Vic
APPLICANT: Ge, Liming
APPLICANT: Plueckthum, Andreas
APPLICANT: Plueckthum, Andreas
APPLICANT: APPLICA
                                                                                                                                                                                       OPERATING SYSTEM: PC-DOS/MS-DOS
SOGTWARE: Patentin Release #1.0, Version #1.25 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 23-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 02-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 02-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9125579.8
FILING DATE: 02-DEC-1991
PRIOR APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
PRIOR APPLICATION NUMBER: GB 920637.6
FILING DATE: 33-SEP-1992
PRIOR APPLICATION NUMBER: GB 952504.9
FILING DATE: 33-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: BCT/GB92/02240
FILING DATE: 01-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: BCT/GB92/02240
FILING DATE: 02-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: BCT/GB92/02240
FILING DATE: 01-JUN-1994
ATTORNEY/AGENT TYRORMATION:
NAME: DAVIG DATE: 01-JUN-1994
ATTORNEY/AGENT TYRORMATION:
NAME: DAVIG DATE: 01-JUN-1994
TELECOMMUNICATION NUMBER: 28111/33308
TELECOMMUNICATION NUMBER: 280 DD N: TELECOMMUNICATION NUMBER: 28111/33308
TELECOMMUNICATION POR SEQ DD N: 15:
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STATE: Illinois
COUNTRY: United States of America
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TYPE: amino acid
TOPOLOGY: linear
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Best Local Similarity 100.
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
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COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-MG-1995
ATTORNEY/AGENT INPORMATION:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATINE SYSTEM: PC-DOS/MS-DOS
OPERATINE SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PALENTIN Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
RECISTRATION NUMBER: 27,794
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFORMUNICATION INFORMATION:
TELEFORMUNICATION NUMBER: 27,794
TELEFAX: (212)596-9000
TELEFAX: (212)596-9000
INPORMATION POR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Score 35; DB 3; Length 112; ; Pred. No. 1.9;
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; Sequence 19, Application US/09490070A
; Sequence 19, Application US/09490070A
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
Pack, Peter
; ITLE OF INFORMATION:
; Moroney, Simon
Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly) peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
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Gaps
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COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: DAY COMPATIBLE
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,324
FILING DATE: 24-3a-2000
PRIOR APPLICATION NUMBER: US/09/025,769
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
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ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave STRET: 1251 Avenue of the Americas CITY. New York STATE: New York COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 35; DB 4; Length 112;
                                 Length 112;
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                                                                                                                                                                                                                                                                                                         APPLICANT: Knappik, Achim
Pack, Peter
Ilag, vic
Ge, Liming
Moroney, Simon
Pluckthun, Andreas
TITLE OF INVENTION: Protein/(Poly) peptide libraries
                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: James F. Haley, Jr., Esq. REGISTRATION NUMBER: 27,794 REFERENCE/DOCKET NUMBER: MORPHO/5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-490-324-19
                                                                                                                                                                                                                                                   Sequence 19, Application US/09490324
Patent No. 6828422
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
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                                   100.0%;
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COMPUTER READABLE FORM:
                                   Query Match 100.
Best Local Similarity 100.
Matches 7; Conservative
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Best Local Similarity 100.
Matches 7; Conservative
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52 DVSKRPS 58
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US-09-383-667-25
US-09-490-153-19
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US-09-490-324-19
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,153
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95
FILING DATE: 18-AUG-1995
                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave STREET: 1251 Avenue of the Americas CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 19, Application US/09490153

Patent No. 6706484

GENERAL INFORMATION:

APPLICANT: Knappik, Achim
Pack, Peter

Ilag, Vic

Ge, Liming
Moroney, Simon
Plueckthun, Andreas

TITLE OF INVENTION: Protein/(Poly) peptide libraries

NUMBER OF SEQUENCES:

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                 Length 112;
                                                                                                                                                                                                                                                                                                                                                      0; Indels
            REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37629-0005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 912-2000
TELEPHONE: (202) 912-2000
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                               DB 4;
                                                                                                                                                                                                                                                                                                               100.0%; Score 35; DB 4
                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
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NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                 STRANDEDNESS: «Unknown»
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-490-070A-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: «Unknown»
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 19:
NAME: Colin G. Sandercock, Esg.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (212)596-9000
TELEPAX: (212)596-9090
INFORMATION FOR SEQ ID No. 19:
SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: New York COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                    52 DVSKRPS 58
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APPLICANT: LEWIS, ALAN PETER
TITLE OF INVENTION: PRODUCTION OF ANTIBODIES
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: ROTHWELL, FIGG, ERNST & KURZ
STREET: 555 THIRTERNTH ST. N.W.
CITY: WASHINGTON
STATE: D. C.
COUNTRY: U.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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; Sequence 125, Application US/09424840B
; Patent No. 6790938
; GENERAL INFORMATION:
APPLICANT: Berchtchd, Peter
APPLICANT: Berchtchd, Peter
TITLE OF INVENTION: ANT-GPIIB/IIIA RECOMBINANT ANTIBODIES
FILE REFERENCE: 100564-09049
; CURRENT APPLICATION NUMBER: US/09/424,840B
; CURRENT FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: DE 19820663.1
; PRIOR PELING DATE: 1998-05-08
; PRIOR FILING DATE: 1997-06-06
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 128
; SEQ ID NOS: 128
; SEG ID NOS: 128
                                       GENERAL INFORMATION:
APPLICANT: Adams, Camelia W.
APPLICANT: Adams, Camelia W.
APPLICANT: Barant: Brigitte
APPLICANT: Barant: Brigitte
APPLICANT: Barant: Brigitte
APPLICANT: Barant: Brigitte
APPLICANT: Wordce, J. Kevin
APPLICANT: Kirchofer. Daniel
APPLICANT: Kirchofer. Daniel
APPLICANT: Suggett, Shelley
TITE OF INVENTION: Human Anti-Factor IX/IXa Antibodies
FILE REFERENCE: P1661R2
CURRENT APPLICATION NUMBER: US/09/383,667
CURRENT APPLICATION NUMBER: US 60/098,233
EARLIER APPLICATION NUMBER: US 60/098,233
SEALLER APPLICATION NUMBER: US 60/098,233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 31; DB 4; Length ', Pred. No. 4.18+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88.6%; Score 31; DB 4; Length 7; 85.7%; Pred. No. 4.1e+05; ive 1; Mismatches 0; Indels
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Best Local Similarity 85.7
Matches 6; Conservative
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Matches 6; Conservative
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CORGANISM: Homo sapiens
US-09-383-667-25
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1 EVSKRPS 7
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COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,550
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
                                                                                                                       OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/378,939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS STREET: 699 Prince Street
CIIY: Alexandria
                                                                                                                                                                                                                                                                      APPLICATION ......
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/952640
FILING DATE: 01-DEC-1992
ATTORNEY/ACENT INFORMATION:
NAME: ERNST, BARBARA G
REGISTRATION NUMBER: 30,377
REFERENCE/DOCKET NUMBER: 1808-118
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (202) 783-6040
TELEFAX: (202) 783-603;
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : 235 amino acids
amino acid
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , MOLECULE TYPE: protein US-08-378-939-12
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nes 6; Conserv
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Best Local $
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US-08-378-939-12; Application US/08378939; Sequence 12, Application US/08378939; Patent No. 2876961.
GENERAL INFORMATION: APPLICANT: CROWE, JAMES SCOTT

Gaps

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Indels

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Mismatches

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5; Conservative
Matches
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TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
TITLE OF INVENTION: IMMUNOSUPPRESANTS"
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
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                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                      Score 31; DB 3; Length 236;
Pred. No. 33;
                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/526,098
                                                                                                                                                                                                                                                                                                                                              2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
PRIOR APPLICATION:
APPLICATION NUMBER: 09/383,916
FILING DATE:
PILING DATE: 07-UN-1995
FILING DATE: 07-UN-1995
ATORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 35,037
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
                               35,030
FR: 012712-131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 10, Application US/09526098
Patent No. 6492134
GENERAL INFORMATION:
            NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REPERSOR/DOCKET NUMBER: 0127
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEPHONE: 703-836-6221
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 236 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 236 amino acids
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 71.4
Matches 5; Conservative
                                                                                                                                                                                              TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-487-550-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
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71 DINKRPS 77
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COUNTRY: USA
ZIP: 22314
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STATE:
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88.6%; 71.4%;

Query Match Best Local Similarity

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APPLICANT: Anderson, Darrell R.

TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
TITLE OF INVENTION: IMMUNOSUPPRESANTS"
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
STATE OF SEQUENCES: STATE OF SEQUENCE ADDRESSER STATE OF SEQUENCES. STATE OF SEQUENCE ADDRESSER STATE OF SEQUENCE OF SECUENCE OF SEQUENCE OF SEQU
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US-09-949-016-7859
Squence 7859, Application US/09949016
Squence 7859, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: PUTH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
CURRENT PELLING AND ADDISONATION NUMBER: 60/241,755
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
RILING DATE: 26-AUG-1999
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS STREET: 699 Prince Street CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 33;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/487,550
FILING DATE: 07-001-1995
ATORNEY/AGRAT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-131
TELEPHONE: 703.836-6620
                                                                                                                                                                                                                                       US-09-383-916-10
; Sequence 10, Application US/09383916
; Patent No. 6709554
; GENERAL INFORMATION:
APPLICANT: Anderson, Darrell R.
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MEDIUM TYPE: Floppy disk
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Best Local Similarity 71..*
Local 5; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 236 amino acids
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71 DINKRPS 77
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71 DINKRPS 77
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1 DVSKRPS 7
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Search completed: October 14, 2005, 16:22:03 Job time : 14.7812 secs
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Sequence 13, Application US/09369364A
Sequence 13, Application US/09369364A
Sequence 13, Application US/09369364A
GENERAL INFORMATION:
APPLICANT: Hurskainen, Tiina L.
APPLICANT: Hurskainen, Tiina L.
APPLICANT: Hurshainen, Talona L.
APPLICANT: Hurshainen, Talona L.
APPLICANT: Hurshainen, Talona L.
APPLICANT: Hurshainen, Talona L.
CURRENT APPLICATION NUMBER: US/09/369,364A
CURRENT APPLICATION NUMBER: US/09/369,364A
NUMBER OP SEQ ID NOS: 31
SOFTWARE: PatentIn Ver. 2.1
SOFTWARE: PatentIn Ver. 2.1
TYPE: PRT
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                    88.6%; Score 31; DB 4; Length 1039; 100.0%; Pred. No. 1.6e+02; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 33, Application US/09025769B
; Patent No. 6300064
; Patent No. 6300064
; Patent No. 6300064
; APPLICANT: Rnappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Pack, Peter
; APPLICANT: Moroney, Simon
; APPLICANT: Moroney, Simon
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens ADAMTS-9
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LOCATION: (468)
OTHER INFORMATION: Xaa = C
NAME/KEY: MOD RES
LOCATION: (521)
OTHER INFORMATION: Xaa = Y
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Best Local Similarity 100.
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                 1 DVSKRP 6
                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Human
                                                                                                                                                                                                                                                                          US-09-949-016-7859
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US-09-369-364A-13
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US-09-025-769B-33
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MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Patentin Release #1.0, Version #1.30 (EPO)
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
PRIOR APPLICATION DATA:
APPLICATION UNDRER: EP 95 11 3021.0
PILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., ESG.
REGISTRATION NUMBER: 27,794
REFERENCE/POCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 30; DB 3; Length 110;
Pred. No. 25;
0; Mismatches 1; Indels
1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 110 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 85.7%;
Matches 6; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     f: 110 amino acids amino acid
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                                CITY: New York
STATE: New York
                                                                                                        USA
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                                                                                                        COUNTRY:
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Sequence Seq

Sequence Sequence Sequence

US-09-880-748-1927
US-10-2914-18-1927
US-10-981-692-39
US-10-981-692-39
US-09-880-692-36
US-10-293-418-1926
US-10-293-418-1926
US-10-293-418-1926
US-10-981-692-36
US-10-981-692-36
US-09-880-748-1913
US-09-880-748-1913
US-09-880-748-1913
US-09-880-748-1682
US-09-880-748-1682
US-09-880-748-1682
US-09-880-748-1682
US-10-293-418-1928
US-10-293-290-46

Sequence

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Sequence Sequence Sequence Sequence

ALIGNMENTS

Sequence

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Sequence 98, Appl
Sequence 1, Appl
Sequence 61, Appl
Sequence 61, Appl
Sequence 1898, Ap
Sequence 1898, Ap
Sequence 2055, Ap
Sequence 2055, Ap
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                                                                                                                                October 14, 2005, 16:20:10 ; Search time 49.7656 Seconds (without alignments) 58.615 Million cell updates/sec
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/ (cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
/ (cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
/ (cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
/ (cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
/ (cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
/ (cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
/ (cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
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/ (cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
/ (cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
/ (cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
/ (cgn2_6/ptodata/2/pubpaa/US16_PUBCOMB.pep:*
GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd
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US-10-453-668-98
US-10-347-331-1
US-10-360-828-61
US-10-916-758-42
US-09-880-748-1898
US-10-293-418-1898
US-10-293-418-2055
US-10-981-652-44
US-10-981-652-44
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                      1859788 segs, 416717961 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Published Applications AA:*
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Maximum Match 100%
Listing first 45 summaries
                                                                                             protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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Maximum DB
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100.0%; Pred. No. 15;
ive 0; Mismatches 0;
gequence 98, Application US/10308817
; Publication No. US20030219861A1
; GENERAL INFORMATION:
; APPLICANT: Rother, Russell
; APPLICANT: Rother, Russell
; APPLICANT: Wu, Dayang
; TITLE OF INVENTION: HYBRID ANTIBODIES
; FILE REFERENCE: 1087-37
; CURRENT APPLICATION NUMBER: US/10/308,817
; CURRENT FILING DATE: 2002-12-03
; NUMBER OF SEQ ID NOS: 195
; SEQ ID NO 98
; LENGTH: 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-453-698-98
; Sequence 98, Application US/10453698
; Publication No. US20040038308A1
; Publication No. WS20040038308A1
; APPLICANT: Rother, Russell
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100.0%;
Best Local Similarity 100.0%;
Matches 7; Conservative 0
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US-10-308-817-98
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RESULT 6
US-09-880-748-1898
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Sequence 61, Application US/10360828

Publication No. US2030206909A1

GENERAL INFORMATION:
APPLICANT: Hua, Shaobing

APPLICANT: Hua, Shaobing

TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES AGAINST MEMBRANE PROTEINS

FILE REFERENCE: 2563-727

CURRENT APPLICATION NUMBER: US/10/360,828

CURRENT FILING DATE: 2003-02-07

PRIOR PILING DATE: 2002-02-08

PRIOR FILING DATE: 2002-04-25

NUMBER OF SEQ ID NOS: 64
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100.0%; Score 35; DB 15; Length 110;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 7; Conservative 0; Mismatches 0; Indels (
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Sequence 1. Application US/10447331

Publication No. US20030219434A1

GENERAL INFORMATION:

APPLICANT: Carter, Paul J.

APPLICANT: Carter, Paul J.

TITLE OF INVENTION: ANTIBODIES FOR CANCER THERAPY AND TITLE OF INVENTION: DIAGNOSIS

FILE REFERENCE: GENENT.1.22A

CURRENT APPLICATION NUMBER: US/10/447,331

CURRENT FILING DATE: 2003-05-28

PRIOR FILING DATE: 2000-02-29

PRIOR FILING DATE: 1999-03-01

NUMBER OF SEQ ID NOS: 6

SOFTWARE: FattSEQ for Windows Version 4.0

SEALOND 11.
TITLE OF INVENTION: HYBRID ANTIBODIES FILE REFERENCE: 82 CIP (1087-37 CIP) CURRENT APPLICATION NUMBER: US/10/453,698 CURRENT FILING DATE: 2003-06-03 NUMBER OF SEQ ID NOS: 196 SOFTWARE: Patentin version 3.2 SEQ ID NO 98 LENGTH: 99
                                                                                                                                                                                                                                   ; LENGTH: 110
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-447-331-1
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ORGANISM: human
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                                                                                                                              100.0%; Score 35; DB 15;
100.0%; Pred. No. 17;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 35; DB 18;
100.0%; Pred. No. 18;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                   Sequence 42, Application US/10916758
; Sequence 42, Application US/10916758
; Publication No. US20050180977A1
; GENERAL INFORMATION:
; APPLICANT: Madison, Edwin L.
; TITLE OF INVENTION: ENDOTHELIASE-2 LIGANDS
; FILE REFERENCE: 10280-065001
; CURRENT APPLICATION NUMBER: US/10/916,758
; CURRENT PILING DATE: 2004-08-12
; PRIOR APPLICATION NUMBER: US 60/520,164
; PRIOR APPLICATION NUMBER: US 60/520,164
; PRIOR FILING DATE: 2003-10-14
; PRIOR FILING DATE: 2003-08-14
; NUMBER OF SEQ ID NOS: 113
; SEQ ID NO 42
: LENGTH: 118
                                                                                    ; OTHER INFORMATION: VL of scFv Ab124
US-10-360-828-61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
SOFTWARE: Patentin version 3.1
SEQ ID NO 61
LENGTH: 111
                                         TYPE: PRT
ORGANISM: Artificial Sequence
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Matches 7; Conservative
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Best Local Similarity
Matches 7; Conserv
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Gaps

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Sequence 24, Application US/10981692
Publication No. US20050163777A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Antibodies that Specifically Bind to Neurokinin B
FILE REFERENCE: PF590P1
CURRENT APPLICATION NUMBER: US/10/981,692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2055, Application US/10293418

Publication No. US20030223996A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REFERENCE: PF523P2

CURRENT APPLICATION NUMBER: US/10/293,418

CURRENT APPLICATION NUMBER: 06/331,469

PRIOR APPLICATION NUMBER: 60/331,469

PRIOR APPLICATION NUMBER: 06/340,817

PRIOR FILING DATE: 2001-12-19

PRIOR FILING DATE: 2001-12-19

PRIOR FILING DATE: 2001-05-25

PRIOR FILING DATE: 2001-05-25

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-16

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR FILING DATE: 2001-03-16

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR APPLICATION NUMBER: 60/210,016

PRIOR PRIOR APPLICATION NUMBER: 60/210,016

PRIOR PRIOR PRIOR DATE: 2000-00-10-17

PRIOR FILING DATE: 2000-00-16

PRIOR FILING DATE: 2000-00-16
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PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR PILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2055
LENGTH: 241
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Best Local Similarity 100.
Matches 7; Conservative
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Best Local Similarity 100.
Matches 7; Conservative
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; ORGANISM: Homo sapiens
US-10-293-418-2055
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US-09-880-748-2055
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US-10-981-692-24
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APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REPERENCE: PF523P2

CURRENT APPLICATION NUMBER: US/10/293,418

CURRENT APPLICATION NUMBER: US/31,469
PRIOR PILING DATE: 2001-11-16

PRIOR PELLING DATE: 2001-11-16

PRIOR PLILING DATE: 2001-12-19

PRIOR PLILING DATE: 2001-06-15

PRIOR PLILING DATE: 2001-06-15

PRIOR PLILING DATE: 2001-06-15

PRIOR PLILING DATE: 2001-06-15

PRIOR PPLICATION NUMBER: 06/277,379

PRIOR PLILING DATE: 2001-03-21

PRIOR PLILING DATE: 2001-03-16

PRIOR PLILING DATE: 2001-03-16

PRIOR PLILING DATE: 2001-03-16

PRIOR PLILING DATE: 2000-06-16

PRIOR PLILING DATE: 2000-01-17

PRIOR PLILING DATE: 2000-06-16

NUMBER OF SEQ ID NOS: 3247
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; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
; FILE REPERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR PLING DATE: 2000-06-15
; PRIOR PLING DATE: 2000-06-15
; PRIOR PLING DATE: 2000-10-17
; PRIOR PLING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/240,816
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1898
LENGTH: 240
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                                                                                      ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1898
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US-10-293-418-1898
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181 DVSKRPS 187
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PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: Patentin Ver. 2.0
SERVID NO 1927
LENGTH: 243
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; Publication No. US20030223996A1
; GENERAL INFORMATION:
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Best Local Similarity 100.
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                                                                                                                                                                                      TYPE: PRT
CAGANISM: Homo sapiens
US-09-880-748-1927
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| Sequence 40, Application to US/20050163777A1
| Sequence 40, Application to US/20050163777A1
| GENERAL INFORMATION:
| APPLICANT: Rosen et al. |
| TITLE OF INVENTION: Antibodies that Specifically Bind to Neurokinin B FILE REFERENCE: PF590P1
| CURRENT APPLICATION NUMBER: US/10/981,692
| CURRENT PELLING DATE: 2004-11-05 |
| PRIOR APPLICATION NUMBER: PCT/US03/16802 |
| PRIOR FILING DATE: 2003-05-29 |
| PRIOR FILING DATE: 2003-05-29 |
| PRIOR FILING DATE: 2005-05-30 |
| NUMBER OF SEQ ID NOS: 76 |
| SEQ ID NO 40 |
| LENGTH: 242
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; APPLICANT: Ruben et al.; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS; PILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15; PRIOR PAPLICATION NUMBER: 60/212,210
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR PILING DATE: 2000-10-17
; PRIOR PILING DATE: 2000-10-17
; PRIOR FILING DATE: 2000-10-17
; PRIOR FILING DATE: 2001-03-16
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Best Local Similarity 100.0%; Score 35; DB 18; Length 242;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 35; DB 18; Length 242; 100.0%; Pred. No. 37; ive 0; Mismatches 0; Indels
  CURRENT FILING DATE: 2004-11-05
PRIOR APPLICATION NUMBER: PCT/US03/16802
PRIOR FILING DATE: 2003-05-29
PRIOR PELLING DATE: 2002-05-30
PRIOR FILING DATE: 2002-05-30
NUMBER OF SEQ ID NOS: 76
SOFTWARE: Patentin version 3.1
LENGTH: 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , OTHER INFORMATION: N015D10 scFv
US-10-981-692-40
                                                                                                                                                                                                                                                                                ) OTHER INFORMATION: N015E08 BCFV
US-10-981-692-24
                                                                                                                                                                                                                                   ORGANISM: Artificial sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial sequence
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Best Local Similarity 100.(
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           182 DVSKRPS 188
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US-10-981-692-40
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GENERAL INVOLVATION:

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF523P2

CURRENT APPLICATION NUMBER: US/10/293,418

CURRENT FILING DATE: 2002-11-27

PRIOR APPLICATION NUMBER: 60/331,469

PRIOR APPLICATION NUMBER: 60/340,817

PRIOR APPLICATION NUMBER: 60/290,980,748

PRIOR PILING DATE: 2001-12-19

PRIOR FILING DATE: 2001-06-15

PRIOR PLICATION NUMBER: 60/293,499

PRIOR PLICATION NUMBER: 60/295,99

PRIOR PLICATION NUMBER: 60/296,248

PRIOR APPLICATION NUMBER: 60/206,248

PRIOR PLILING DATE: 2001-03-21

PRIOR PLILING DATE: 2001-03-21

PRIOR PLILING DATE: 2001-03-21

PRIOR PLILING DATE: 2000-06-16

PRIOR PLILING DATE: 2000-06-16
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100.0%; Score 35; DB 10; Length 243; 100.0%; Pred. No. 37; ive 0; Mismatches 0; Indels (
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100.0%; Score 35; DB 15; Length 243;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 7; Conservative 0; Mismatches 0; Indels
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| Publication No. US20050163777A1
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| TITLE OF INVENTION: Antibodies that Specifically Bind to Neurokinin B FILE REFERENCE: PESSOR!
| FILE REFERENCE: PESSOR!
| FILE REFERENCE: PESSOR!
| FILE REFERENCE: PESSOR!
| FRICA PAPLICATION NUMBER: DC7/US03/16802
| PRIOR APPLICATION NUMBER: 60/293,802
| PRIOR APPLICATION NUMBER: 60/383,802
| PRIOR APPLICATION NUMBER: 60/383,802
| PRIOR PRIUG DATE: 2002-05-30
| PRIOR APPLICATION NUMBER: 60/383,802
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Best Local Similarity 100.0%; Pred. No. 37;
Matches 7; Conservative 0; Mismatches 0; Indels (
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PRIOR APPLICATION NUMBER: PCT/US03/16802
PRIOR FILING DATE: 2003-05-29
PRIOR PPLICATION NUMBER: 60/383,802
PRIOR FILING DATE: 2005-05-30
NUMBER OF SEQ ID NOS: 76
SOFTWARE: Patentin version 3.1
LENGTH: 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; FEATURE:
; OTHER INFORMATION: N024E07 scFv
US-10-981-692-29
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; OTHER INFORMATION: N023E01 sCFV
US-10-981-692-33
                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial sequence
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Best Local Similarity 100.
Matches 7; Conservative
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US-10-981-692-33
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Search completed: October 14, 2005, 17:00:44 Job time : 50.7656 secs

183 DVSKRPS 189

1 DVSKRPS 7

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GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
                Copyright
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- protein search, using sw model OM protein October 14, 2005, 15:51:19; Search time 84.5625 Seconds (without alignments) 50.310 Million cell updates/sec Run on:

US-10-614-959-15 58

1 AAWDDSLSEFL 11 score: Perfect sc Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2105692 segs, 386760381 residues Searched:

2105692 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

genesqp1980s:* genesqp2000s:* genesqp2001s:* genesqp2001s:* genesqp2002s:* genesqp2003bs:* genesqp2003bs:* A Geneseq 16Dec04:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Score Macch Length DB ID  Search Look	Regult		Otterry				
1         58         100.0         11         3         AAY79073         Aay79073         Aay79073           2         58         100.0         104         2         AAR80087         Aax80087         Aax80087           4         58         100.0         110         4         AAU02544         Aau02548         Aau02548           5         100.0         110         4         AAU02512         Aau02558         Aau02551           6         58         100.0         110         4         AAU02627         Aau02622           9         58         100.0         111         4         AAU02629         Aaw19883           10         58         100.0         111         4         AAU02629         Aaw19883           11         58         100.0         111         4         AAU02651         Aaw19883           12         58         100.0         111         4         AAU02551         Aav19883           13         58         100.0         111         4         AAU02666         Aav19883           14         58         100.0         243         5         ABP45916         Aav19883           15         58		Score	Match	Length	DB	ΙD	Description
2         58         100.0         104         2         AAB80087         Aag8087           3         58         100.0         104         2         AAB80687         Aav85485         Aav85485           5         100.0         110         4         AAU02544         Aau02548         Aau02548           6         58         100.0         110         4         AAU02612         Aau02652           7         58         100.0         110         4         AAU02627         Aau02627           8         100.0         111         2         AAV1983         Aav19883           9         58         100.0         111         4         AAU02627         Aav19883           10         111         2         AAV19833         Aav19883         Aav19883           1         4         AAU02652         Aav19883         Aav19883           1         4         AAU02555         Aav19883         Aav19883           1         4         AAU02656         Aav19883         Aav19883           1         4         AAU026585         Aav19883         Aav19883           2         1         1         AAU02666         Aav19883 <td>-</td> <td>58</td> <td>100.0</td> <td>11</td> <td><u>_</u> ۳</td> <td>AAY79073</td> <td>Aay79073 Anti-fact</td>	-	58	100.0	11	<u>_</u> ۳	AAY79073	Aay79073 Anti-fact
3         58         100.0         104         2         AAM95485         Aaw95485           4         58         100.0         110         4         AAU02544         Aau02554           5         100.0         110         4         AAU02612         Aau02562           7         58         100.0         110         4         AAU02627         Aau02627           9         58         100.0         111         2         AAW1983         Aaw1983           10         111         2         AAW1983         Aaw1983           10         111         4         AAU02542         Aaw19883           10         111         4         AAU02542         Aaw19883           10         111         4         AAU02542         Aaw19883           10         111         4         AAU02551         Aaw19883           10         111         4         AAU02551         Aau02562           2         100.0         242         8         ADG34301         AdG34331           4         58         100.0         243         5         ABP45916         AdG34310           5         100.0         243         8	7	58	100.0	104	~	AAR80087	
4         58         100.0         109         4 AAU02554         Aau02544           5         5         100.0         110         4 AAU02558         Aau02655           7         5         100.0         110         4 AAU02659         Aau02627           8         5         100.0         111         2 AAM1983         Aau02627           9         5         100.0         111         4 AAU02551         Aau02627           1         5         100.0         111         4 AAU02551         Aau02642           1         5         100.0         111         4 AAU02551         Aau02642           2         5         100.0         111         4 AAU02551         Aau02642           3         100.0         111         4 AAU02551         Aau02665           4         5         100.0         111         4 AAU02666         Aau02666           5         100.0         242         8 ADG34301         AdG34301         AdG34310           6         5         100.0         243         5 ABP45916         AdG34310         AdG34310           6         5         100.0         243         8 ADG34310         AdG34310         AdG34310	е	28	100.0	104	7	AAW95485	
5         100.0         110         4 AAU02558         Aau02558           6         58         100.0         110         4 AAU02612         Aau02672           8         100.0         110         4 AAU02627         Aau02627           9         58         100.0         111         2 AAM19883         Aau02629           9         58         100.0         111         4 AAU02542         Aau02629           10         111         4 AAU02542         Aau026229         Aau02629           2         100.0         111         4 AAU02542         Aau026229           3         58         100.0         111         4 AAU02561         Aau02685           3         58         100.0         242         8 ADG34317         Adg34317           4         58         100.0         242         8 ADG34317         Adg34317           5         100.0         243         7 ADG36743         Adg34310           6         58         100.0         243         8 ADG34306           9         58         100.0         244         8 ADG34306           1         58         100.0         245         AABP45915           2	4		100.0	109	4	AAU02544	4
6         58         100.0         110         4 AMU02612         ABU02627         ABU02627         ABU02627         ABU026262         ABU026262 <t< td=""><td>ß</td><td></td><td>100.0</td><td>110</td><td>4</td><td>AAU02558</td><td></td></t<>	ß		100.0	110	4	AAU02558	
7         58         100.0         110         4 AAU02627         Aau02627           8         58         100.0         111         2 AAW19893         Aaw19863           9         58         100.0         111         4 AAU02551         Aau02642           1         58         100.0         111         4 AAU02551         Aau02642           3         58         100.0         111         4 AAU02551         Aau026542           4         58         100.0         111         4 AAU02666         Aau022651           5         100.0         242         8 ADG34301         Aag34310           6         58         100.0         243         5 ABP45916         AAG34310           6         58         100.0         243         5 ABP45916         AAG34310           7         58         100.0         243         8 ADG34310         AAG34310           8         58         100.0         243         8 ABP45916         AAG34310           9         58         100.0         244         8 ABP45916         AAG34310           1         58         100.0         245         7 ABG88057         AAG986742           2	9		100.0	110	4	AAU02612	7
8         58         100.0         110         4         AAU02629         Aau02629           9         58         100.0         111         2         AAW19883         Aaw19883           10         0         111         4         AAU02542         Aaw19883           1         58         100.0         111         4         AAU02542         Aaw19883           2         58         100.0         111         4         AAU02542         Aaw102543           3         58         100.0         111         4         AAU02565         Aau022655           4         58         100.0         242         8         ADG34317         Adg34317           5         100.0         243         8         ADG34317         Adg34317           6         58         100.0         243         8         ADG34310         Adg34310           9         58         100.0         243         8         ADG34330         Adg34310           1         58         100.0         245         ABP45915         Adg34310           1         58         100.0         245         ABP45916         Adg34310           2         100.0 </td <td>7</td> <td></td> <td>100.0</td> <td>110</td> <td>4</td> <td>AAU02627</td> <td>_</td>	7		100.0	110	4	AAU02627	_
9         58         100.0         111         2         AAM19883         Aaw19883           10         58         100.0         111         4         AAU02542         Aau025542           2         58         100.0         111         4         AAU02565         Aau02551           3         58         100.0         111         4         AAU0266         Aau02565           4         58         100.0         242         8         AbG34310         AdG34310           5         100.0         243         8         AbG34310         AdG34310         AdG34310           6         58         100.0         243         8         AbG34310         AdG34310           9         58         100.0         243         8         AbG34310         AdG34310           10         243         8         AbG34310         AdG34310         AdG34310           10         243         8         AbG34310         AdG34310         AdG34310           1         58         100.0         244         8         AbG34310         AdG34310           2         58         100.0         245         7         AbG96742         AdG94515	æ	28	100.0	110	4	AAU02629	σ.
0         58         100.0         111         4         AAU02552         Aau02542           1         58         100.0         111         4         AAU02551         Aau02585           3         58         100.0         111         4         AAU02666         Aau02685           4         58         100.0         242         8         AAG34301         AAG34310           5         58         100.0         243         8         AAG434301         AAG34310           6         58         100.0         243         5         ABP45916         AAG34311           7         58         100.0         243         8         AAG34310         AAG34311           9         58         100.0         243         8         AAG34310         AAG34310           9         58         100.0         243         8         AAG34310         AAG34310           1         58         100.0         244         8         AAG44303         AAG34310           2         58         100.0         245         7         AAG44303         AAG44310           3         58         100.0         245         7         AAG486742	σ	58	100.0	111	~	AAW19883	m
1         58         100.0         111         4 AAU02551         Aau02255           2         58         100.0         111         4 AAU02685         Aau022685           3         58         100.0         242         8 ADG34301         Adg34301           5         58         100.0         242         8 ADG34317         Adg34317           6         58         100.0         243         5 ABP45916         Adg34311           8         100.0         243         5 ADG34310         Adg34310           9         58         100.0         243         8 ADG34310         Adg34310           9         58         100.0         243         8 ADG34310         Adg34310           10         243         8 ADG34310         Adg34310         Adg34310           10         243         8 ADG34310         Adg34310         Adg34310           10         245         8 ABP45915         Adg34303         Adg34303           1         58         100.0         245         ABP45915         Adg34303           2         58         100.0         245         ABP45915         Adg34303           3         58         100.0         245<	10	58	100.0	111	4	AAU02542	
2         58         100.0         111         4         AAU02585         Aau022885           3         58         100.0         111         4         AAU02606         Aau02606           5         100.0         242         8         AAG34317         Adg34317         Adg34317           6         58         100.0         243         5         ABF45916         Abg45916         Abg45916           7         58         100.0         243         7         ADG96743         Adg34310         Adg34310           9         58         100.0         243         8         ADG34306         Adg34310         Adg34310           1         58         100.0         245         ABP45915         Adg34310         Adg34310           1         58         100.0         245         ABP45915         Adg34310         Adg34310           2         100.0         245         ABP45915         Adg34310         Adg34310           2         100.0         245         ABP45915         Adg34310         Adg34310           3         58         100.0         245         ABP45915         Adg3430           4         58         ADG34308         Ad	11	58	100.0	111	4	AAU02551	_
3         58         100.0         111         4         AAU02606         Aau022606           4         58         100.0         242         8         ADG34301         Adg34310           6         58         100.0         243         5         ABP45916         Abg45316           7         58         100.0         243         7         ABG56743         Adg34317           9         58         100.0         243         8         ADG34310         Adg34310           9         58         100.0         243         8         ADG34310         Adg34310           1         58         100.0         244         8         ADG34303         Adg34310           2         58         100.0         245         7         ADG36742         Adg3430           2         58         100.0         245         7         ADG36742         Adg36742           3         58         100.0         245         7         ADG38057         Adg98057           4         58         100.0         245         8         ADG34308         Adg434308           9         100.0         245         8         ADG34308         Adg434308 </td <td>12</td> <td>28</td> <td>100.0</td> <td>111</td> <td>4</td> <td>AAU02585</td> <td>'n</td>	12	28	100.0	111	4	AAU02585	'n
4         58         100.0         242         8         AbG34301         Adg34301           5         58         100.0         242         8         AbG34317         Adg34317           7         58         100.0         243         7         AbG34317         Abg34516           8         58         100.0         243         8         AbG34310         Adg34516           9         58         100.0         243         8         AbG34310         Adg34310           9         58         100.0         243         8         AbG34310         Adg34310           1         58         100.0         245         5         AbB45915         AbG34303           2         58         100.0         245         7         AbG38057         AbG95742           3         58         100.0         245         8         AbG38057         AbG98057           5         100.0         245         8         AbG38362         AbG683865           5         100.0         245         8         AbG34308         AbG983867	13	28	100.0	111	4	AAU02606	
5         58         100.0         242         8         ADG34317         Adg34317           6         58         100.0         243         5         ABP45916         Abp45516           7         58         100.0         243         5         Abp45916         Adg34317           8         58         100.0         243         8         AbG34310         Adg34310           9         58         100.0         243         8         AbG34306         Adg34303           1         58         100.0         245         8         ABP45915         Abg34303           2         58         100.0         245         7         AbG96742         Adg96742           3         58         100.0         245         7         AbG38057         Adg98057           4         58         100.0         245         8         AbB31862         Adg98057           5         100.0         245         8         AbG31862         Adg981862	14	28	100.0	242	œ	ADG34301	Adg34301 Neurokini
6         58         100.0         243         5         ABP45916         Abp45516           7         58         100.0         243         7         Abg65743         Adg95743           9         58         100.0         243         8         Abg34310         Adg34310           9         58         100.0         243         8         Abg34306         Adg34306           1         58         100.0         245         7         Abg34303         Abg45315           2         58         100.0         245         7         AbG36742         Adg396742           3         58         100.0         245         7         AbG38057         Adg38065           5         100.0         245         8         Abg33362         Adg83862           5         100.0         245         8         Abg33362         Adg83862	15	28	100.0	242	ω	ADG34317	Adg34317 Neurokini
7         58         100.0         243         7         AbG96743         Adg96743           8         58         100.0         243         8         AbG34310         Adg34310           9         58         100.0         244         8         AbG34306         Adg34306           1         58         100.0         245         5         ABP45915         Adg34303           2         58         100.0         245         7         AbG96742         Adg96742           3         58         100.0         245         7         AbG98057         Adg98057           4         58         100.0         245         8         AbB3862         Adg981865           5         100.0         245         8         AbB3862         Adg381865	16	28	100.0	243	Ŋ	ABP45916	Abp45916 Human BLy
8         58         100.0         243         8         ADG34310         Adg34310           9         58         100.0         243         8         ADG34336         Adg34306           1         58         100.0         245         5         ABP45313         Adg34303           2         58         100.0         245         7         ADG96742         ADG945915           3         58         100.0         245         7         ADG38057         AdG98057           4         58         100.0         245         8         ADB3862         AdG88057           5         100.0         245         8         ADG34308         AdG88057	11	58	100.0	243	7	ADG96743	Adg96743 Single ch
9         58         100.0         243         8         ADG34306         Adg34306           1         58         100.0         245         5         ABP45915         ADG34303           2         58         100.0         245         5         ABP45915         ADG45915           2         58         100.0         245         7         ADG96742         ADG96742           3         58         100.0         245         8         ADG38057         ADG98057           4         58         100.0         245         8         ADG34308         ADG34308           5         58         100.0         245         8         ADG34308         ADG34308	18	28	100.0	243	æ	ADG34310	Adg34310 Neurokini
0         58         100.0         244         8         AbG34303         Adg34303           1         58         100.0         245         5         ABP45915         Abp45915           2         58         100.0         245         7         AbG96742         Adg96742           3         58         100.0         245         7         AbG98057         Adg99657           4         58         100.0         245         8         AbB83862         Adg383865           5         58         100.0         245         8         AbG34308	19	28	100.0	243	œ	ADG34306	Adg34306 Neurokini
1         58         100.0         245         5         ABP45915         Abp45915           2         58         100.0         245         7         AbG96742         Adg96742           3         58         100.0         245         7         Abg8057         Adg98057           4         58         100.0         245         8         AbG34308         Adg34308           5         6         6         6         6         7         7         7	20	58	100.0	244	ω	ADG34303	Adg34303 Neurokini
2 58 100.0 245 7 ADG96742 Adg96742 3 58 100.0 245 7 ADG38057 Adg98057 4 58 100.0 245 8 ADG83862 Ade83865 5 58 100.0 245 8 ADG34308 Adg83808	21	58	100.0	245	Ŋ	ABP45915	'n
3 58 100.0 245 7 ADG98057 Adg98057 4 58 100.0 245 8 ADG93862 Ade833862 5 58 100.0 245 8 ADG34308 Adg34308	22	28	100.0	245	7	ADG96742	Adg96742 Single ch
4 58 100.0 245 8 ADE83862 Ade83862 5 58 100.0 245 8 ADG34308 Adg34308	23		100.0	245	7	ADG98057	7
5 58 100.0 245 8 ADG34308 Adg34308	24		100.0	245	ω	ADE83862	
	25	28	100.0	245	ω	ADG34308	Adg34308 Neurokini

	Adg96715 Single ch Adg96498 Single ch Adg96744 Single ch Adg96259 Single ch Adg96750 Single ch Adg96523 Single ch Adg96523 Chemokine
ABP45902 ABP45906 ADB45906 ADG933 ADG98729 ADB83872 ABP45923 ABP45923 ABP45923 ABP45986 ADG30455 ADG30455	ADG96715 ADG96498 ADG96744 ADG96259 ADG96750 ADG96523 ADG96523
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## ALIGNMENTS

Complementarity determining region 3; CDR3; antibody; Gla domain; factor IX/IXIs, blood coagulation; deep venous thrombosis; light chain; arterial thrombosis; unstable angina; post myocardial infarction; coronary artery bypass graft; CABG; stroke; tumour growth; metastasis; percutaneous transluminal coronary angioplasty; PTCA; inflammation; septic shock; hypotension; adult respiratory distress syndrome; ARDS; arterial fibrillation; disseminated intravascular coagulopathy; DIC. Anti-factor IX/IXa antibody L chain V domain CDR3 amino acid sequence. AAY79073 standard; peptide; 11 AA (first entry) 12-JUN-2000 AAY79073; 

Homo sapiens.

WO200012562-A1.

09-MAR-2000

99WO-US019453, 26-AUG-1999; 98US-0098233P. 28-AUG-1998; 03-MAR-1999;

(GETH ) GENENTECH INC

Kirchhofer D; Adams CW, Devaux B, Eaton DL, Hass PE, Judice JK, Suggett S:

WPI; 2000-256595/22.

Novel human anti-Factor IX/IXa antibodies against IX/IXa gamma-carboxyglutamic acid domains useful as anti-coagulant in thrombosis, stroke, and post myocardial infarction.

Claim 8; Fig 2; 84pp; English.

This sequence represents a complementarity determining region 3 (CDR3) of the light chain variable domain of a human anti-factor IX/IXa Gla domain antibody. Factor IXA is a vitamin K dependent plasma serine procease that participates in the blood coagulation pathways. The Gla domain of factor IXa and its zymogen factor IX contains important structural determinants for interaction with high affinity binding sites on vascular endothelial

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the treatment or prophylaxis of thrombotic or coagulopathic diseases or disorders in a mammal for which inhibiting a FIX/IXa mediated event is indicated, e.g. deep venous thrombosis, arterial thrombosis, unstable angina, post myocardial infarction, post surgical thrombosis, coronary artery bypass graft (CABG), percutaneous transluminal coronary angioplasty (FTCA), stroke, tumour growth, invasion or metastasis, inflammation, septic shock, hypotension, adult respiratory distress syndrome (ARDS), arterial fibrillation and disseminated intravascular coagulopathy (DIC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            generating a
in phage
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te= "complimentarity determining region 1"
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.e= "complementarity dtermining region 3"
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                                                                                                                                                                                                                                                                                                                            100.0%; Score 58; DB 3; Length 11; 100.0%; Pred. No. 0.0022; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human derived light chain RT3 phage antibody.
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94. .104
/note= "framework region 4"
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/note= "framework region 1"
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:e= "framework region 2"
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.e= "complementarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR80087 standard; protein; 104 AA.
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Martin MT,
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N-PSDB; AAT04634.
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                                                                                                                                                                                                                                                                              Sequence 11 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-MAR-1994;
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Kenten JH,
                                                                                                                                                                                                                                                                                                                               Query Match
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Disclosure, Fig 20, 133pp, English.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Production of catalytic antibodies displayed on bacteriophages -
comprises generating a gene library of antibody-derived domains inserting
coding into a phage expression vector and isolating the catalytic
              The DNA was used in the prepn. of catalytic antibody (CA) producing acteriophage. The CAs can be used to activate/deactivate a biological function in an animal by enhancing the rate of cleavage, or formation of a specific bond within a mol. in vivo
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Catalytic; antibody; phage display; immunising; phage expression vector;
 phage antibody.
                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                           Human-derived RT3 phage antibody light chain genetic sequence
                                                                                                                               100.0%; Score 58; DB 2; Length 104; 100.0%; Pred. No. 0.023; ive 0; Mismatches 0; Indels
AAT04634 encodes AAR80087 human derived light chain RT3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fitzgerald K, Darsley MJ, Williams RO, Smith R, Kenten JH, Chiswell D, Mccafferty J, Titmas RC;
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                                                                                                                                                                                                                                                                                                                          AAW95485 standard; protein; 104
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                                                                                                                                                                    11; Conservative
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DARSLEY M J.
TITMAS R C.
MARTIN M T.
KENTEN J H.
SMITH R.
FITZGERALD K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MCCAFFERTY J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-105036/09.
                                                                                                                             Query Match
Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            prodrug; scFV; RT3
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                                                                                                  Sequence 104 AA
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antibodies
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(CHIS/) (DARS/) I
(TITM/) (MART/) I
(KENT/) (SMIT/) (SMIT/) (WILZ/)
                                                                                                                                                                                                                                                                                        RESULT 3
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abdominal fat associated with heart disease

Sequence 109 AA;

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AAU02501-AAU02615, and AAU02641-AAU02748 represent the amino acid sequences of anti-adipocyte monoclonal antibody heavy chain, light chain, and heavy chain complementarity determining regions (CRN) of the cand heavy chain complementarity determining regions (CRN) of the invention. The antibodies can be used in the treatment of obesity and obesity related diseases. The antibodies can be used to deliver drugs or pro-drugs directly to the far mass of an obese patient or the antibody can be used as a therapeutic itself. Antibodies binding specifically to adipocytes can be used to activate the immune system to destroy the cells by complement mediated lysis. The antibodies may be labeled with a choice can be used to activate the immune system to destroy the cells by complement mediated lysis. The antibodies may be labeled with a used in methods of diagnosis in human subjects e.g. to determine the presence or level of adipocytes in a cell or tissue sample. The antibodies can be used as an alternative means of treatment for obese patients other than undergoing surgery to remove excess fat. Antibodies con the types of fat deposits can also be produced e.g. intra-
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antibodies; selecting phage display antibodies which bind specifically to the antigen; screening the selected phage display antibodies for catalytic activity to substrate; and isolating the catalytic antibodies, where the phage expression vector incorporates a histidine peptide in tandem with a myc peptide. The processes are used to produce catalytic sequences which can be used for in vivo activation of a producy. Sequences AAW95484-489 represent genetic sequences of heavy and light chains of RT3 specific phage antibodies selected from a naive human phage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Panel of specific binding members of antibody molecules which bind to whole adipocytes is used in the treatment of obesity and obesity related
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                                                                                                                                                                                                                                           Score 58; DB 2; Length 104;
Pred. No. 0.023;
Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Anti-adipocyte monoclonal antibody light chain, FAT 31.
                                                                                                                                                                                                                                           100.0%; Score 58; DB
100.0%; Pred. No. 0.0
tive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAU02544 standard; protein; 109 AA.
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Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                          1 AAWDDSLSEFL 11
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                                                                                                                                                                    antibody library
                                                                                                                                                                                                             Sequence 104 AA;
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AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
and heavy chain complementarity determining regions (CDR) of the
cinvention. The antibodies can be used in the treatment of obesity and
cinvention. The antibodies can be used to deliver drugs or
pro-trugs directly to the fat mass of an obese patient or the antibody
can be used as a therapeutic itself. Antibodies binding specifically to
adipocytes can be used to activate the immune system to destroy the cells
con persence of adiapocial properties of the antibodies and methods of diagnosis in human subjects e.g. to determine the
cused in methods of diagnosis in human subjects e.g. to determine the
confidence of adipocyte antigen on the surface of an adipocyte to detect or
determine the presence or level of adipocytes in a cell or tissue sample.
The antibodies can be used as an alternative means of treatment for obese
confidence of diagnosis can also be produced e.g. intra-
abdominal fat associated with heart disease
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Score 58; DB 4; Length 109;
Pred. No. 0.024;
                                  0; Indels
                                                                                                                                                                                                                                                                                                                           Antibody; adipocyte; heavy chain; light chain; obesity; heart disease; complementarity determining region; CDR.
                                                                                                                                                                                                                                                                                          Anti-adipocyte monoclonal antibody light chain, FAT 44.
                                  Mismatches
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                                                                                                                                                                                        AAU02558 standard; protein; 110 AA.
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 100.0%;
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            Local Similarity 100
nes 11; Conservative
                                                                                                    90 AAWDDSLSEFL 100
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                                                                     1 AAWDDSLSBFL
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N-PSDB; AAS03458.
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                                                                                                                                                                                                                                                                                                                                                                                                                 WO200127279-A1.
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                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
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                                                                                                                                                                                                                          AAU02558;
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 Query Match
                   Best Loca
Matches
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AMU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid sequences of anti-adipocyte monoclonal antibody heavy chain, light chain, and heavy chain complementarity determining regions (CDR) of the invention. The antibodies can be used in the treatment of obesity and obesity related diseases. The antibodies can be used to deliver drugs or pro-drugs directly to the fat mass of an obese patient or the antibody can be used as a therapeutic itself. Antibodies binding specifically to adipocytes can be used to activate the immune system to destroy the cells by complement mediated lysis. The antibodies may be labeled with a detectable label such as radiolabel, fluorescent or chemical group and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       used in methods of diagnosis in human subjects e.g. to determine the presence of adipocyte and adipocyte to detect or determine the presence or level of adipocytes in a ciploryte to detect or The antibodies can be used as an alternative means of treatment for obese patients other than undergoing surgery to remove excess fat. Antibodies for different types of fat deposits can also be produced e.g. intra-abdominal fat associated with heart disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Panel of specific binding members of antibody molecules which bind to whole adipocytes is used in the treatment of obesity and obesity related
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                                                                                                                                                               Antibody; adipocyte; heavy chain; light chain; obesity; fat; heart disease; complementarity determining region; CDR.
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                                                                                                                   Anti-adipocyte monoclonal antibody light chain, FAT 112.
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                                                                       (first entry)
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Best Local Similarity
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                           AAU02627;
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                                                                                                                                                                                                                                                                                                              Anti-adipocyte monoclonal antibody light chain, FAT 99.
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                                                                                                                                                                  AAU02612 standard; protein; 110 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 163; 182pp; English.
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ses 11; Conservative
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90 AAWDDSLSEFL 100
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1 AAWDDSLSEFL 11
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Panel

Query Match

Matches

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AAU02627 ID AAU0 RESULT 7

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95GB-00025004
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Matches 11; Conservative
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                                                                                                                                                                                                                                                                     N-PSDB; AAT72133
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                                                                                  WO9720932-A1.
                                                                                                                                  09-DEC-1996;
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                                                                                                                                                          07-DEC-1995;
                                                                                                                                                                                 11-0CT-1996;
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                                     Region
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sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
and heavy chain complementarity determining regions (CDR) of the
invention. The antibodies can be used in the treatment of obesity and
cobesity related diseases. The antibodies can be used to deliver drugs or
pro-drugs directly to the far mass of an obese patient or the antibody
can be used as a therapeutic itself. Antibodies binding specifically to
cappement mediated lysis. The antibodies binding specifically to
by complement mediated lysis. The antibodies binding specifically to
cappement mediated lysis. The antibodies binding any be labeled with a
cdetectable label such as radiolabel, fluorescent or chemical group and
used in methods of diagnosis in human subjects e.g. to determine the
cdetermine the presence or level of adipocytes in a cell or tissue sample.
The antibodies can be used as an alternative means of treatment for obese
patients other than undergoing surgery to remove excess fat. Antibodies
for different types of fat deposite can also be produced e.g. intra-
abdominal fat associated with heart disease
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                                                                                                                                                                                                                               Panel of specific binding members of antibody molecules which bind to whole adipocytes is used in the treatment of obesity and obesity related
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 58; DB 4; Length 110; 100.0%; Pred. No. 0.024; ive 0; Mismatches 0; Indel8
heart disease; complementarity determining region; CDR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CEA-specific antibody CEA1, CEA2, CEA3 VL sequence.
                                                                                                                                             (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY
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                                                                                                                                                                     Vaughan TJ;
                                                                                                                                                                                                                                                                                 Claim 1; Page 173; 182pp; English
                                                                                                                     99US-0158812P.
                                                                                             11-OCT-2000; 2000WO-GB003900.
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/label= CDR1
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108 11; Conservative
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                                                                                                                                                                     Main SH,
                                                                                                                                                                                              WPI; 2001-282031/29
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                      Ното варіепв
                                                                                                                     12-OCT-1999;
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This polypeptide sequence comprises the light chain variable region (VL) of human carcinoembryonic antigen (hCEA) specific antibodies CEA1, CEA2 and CEA3. WH (AAT72123-35) gene sequences were obtained for anti-hCEA antibodies CEA1-CEA7 (see AAM19876-85). A claimed specific binding member (A) comprises an hCEA specific antibody antigen binding domain that has a dissociation constant for hCEA of less than 1 x 10 -8 M, is non-cross-reactive with human liver cells, and preferentially binds to the A3-83 extracellular domain of hCEA and/or to cell-associated hCEA over hCEA over soluble hCEA. Preferred (A) include pairings of VH and VL sequences from CEA1-Y, or their CEN sequences, as well as CEA6 WH and VL variants. (A) is used to detect cells expressing hCEA, in vivo or in vitro, especially tumour cells for diagnosing cancer, e.g. adenocarcinoma of the colon, lung or breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Specific binding members for human carcinoembryonic antigen - bind to the A3-B3 extracellular domain of hCEA and are substantially non-cross-reactive with human liver cells; used for diagnosing cancer.
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50. .56
/label= CDR2
/note= "complementarity determining region 2"
00. .100
/label= CDR3
/note= "complementarity determining region 3"
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AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
and heavy chain complementarity determining regions (CDR) of the
cinvention. The antibodies can be used in the treatment of obesity and
cobesity related diseases. The antibodies can be used to deliver drugs or
pro-drugs directly to the fat mass of an obese patient or the antibody
can be used as a therapentic itself. Antibodies binding specifically to
adipocytes can be used to activate the immune system to destroy the cells
by complement mediated lysis. The antibodies may be labeled with a
cused in methods of diagnosis in human subjects e.g. to determine the
cused in methods of diagnosis in human subjects e.g. to determine the
presence of adipocyte antigneon on the surface of an adipocyte to detect or
determine the presence or level of adipocytes in a cell or tissue sample.
CT the antibodies can be used as an alternative means of treatment for obese
can thought the than undergoing surgery to remove excess fat. Antibodies
cfor different types of fat deposits can also be produced e.g. intra-
abdominal fat associated with heart disease
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                                                                                  Panel of specific binding members of antibody molecules which bind to whole adipocytes is used in the treatment of obesity and obesity related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antibody; adipocyte; heavy chain; light chain; obesity; fat; heart disease; complementarity determining region; CDR.
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100.0%; Pred. No. 0.025;
tive 0; Mismatches 0; Indels
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                                                                                                                                                                                    Claim 1; Page 124; 182pp; English,
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                    2001-282031/29
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                    WPI; 2001-282031
N-PSDB; AAS03451
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                               sequences of anti-adipocyte monoclonal antibody heavy chain, light chain, and heavy chain complementarity determining regions (CDR) of the invention. The antibodies can be used in the treatment of obesity and obesity related diseases. The antibodies can be used to deliver drugs or pro-drugs directly to the fat mass of an obese patient or the antibody can be used as a therapeutic itself. Antibodies binding specifically to adipocytes can be used to activate the immune system to destroy the cells by complement mediated lysis. The antibodies may be labeled with a detectable label such as radiolabel, fluorescent or chemical group and used in mathods of diagnosis in human subjects e.g. to determine the presence of adipocyte antigen on the surface of an adipocyte to detect or determine the presence or level of adipocytes in a cell or tissue sample.
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                                                                                                                                                                                                                                                                              Panel of specific binding members of antibody molecules which bind to whole adipocytes is used in the treatment of obesity and obesity related
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                                                                                                              (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 118-119; 182pp; English.
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N-PSDB; AAS03442.
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                     AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
and heavy chain complementarity determining regions (CDR) of the
invention. The antibodies can be used in the treatment of obesity and
conversely related diseases. The antibodies can be used to deliver drugs or
pro-drugs directly to the fat mass of an obese patient or the antibody
can be used as a therapeutic itself. Antibodies binding specifically to
can be used to activate the immune system to destroy the cells
by complement mediated lysis. The antibodies binding specifically to
detectable label such as radiolabel; fluorescent or chemical group and
considered in methods of diagnosis in human subjects e.g. to determine the
presence of adipocyte antigen on the surface of an adipocyte of the consideration of the antibodies can be used as an alternative means of treatment for obese
considered than undergoing surgery to remove excess fat. Antibodies
considered with heart disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid sequences of anti-adipocyte monoclonal antibody heavy chain, light chain, and heavy chain complementarity determining regions (CDR) of the invention. The antibodies can be used in the treatment of obesity and obesity related diseases. The antibodies can be used to deliver drugs or pro-drugs directly to the fat mass of an obese patient or the antibody
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                                                                                                                                                                                                                                                                                                                                     0; Mismatches
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Claim 1; Page 146; 182pp; English.
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Best Local Similarity 100.
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N-PSDB; AAS03506.
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can be used as a therapeutic itself. Antibodies binding specifically to adjocytes can be used to activate the immune system to destroy the cells by complement mediated lysis. The antibodies may be labeled with a detectable label such as radiolabel, fluorescent or chemical group and used in methods of diagnosis in human subjects e.g. to determine the presence of adjocyte antigen on the surface of an adjocyte to detect or determine the presence or level of adjocytes in a cell or tissue sample. The antibodies can be used as an alternative means of treatment for obese patients other than undergery to remove excess fat. Antibodies for different types of fat deposits can also be produced e.g. intra-abdominal fat associated with heart disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91 AAWDDSLSEFL 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 AAWDDSLSEFL 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rosen CA, Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2004-053456/05.
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Best Local Similarity
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nes 11; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 111 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 242 AA;
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221 AAWDDSLSEFL 231

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                                                                                                                                                                                                                                                                                                                                                                                                                             New antibody that specifically binds neurokinin B, useful for preparing a composition for treating or preventing hypertension or preeclampsia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                         antibody; neurokinin B; hypotensive; gynaecological; gene therapy; hypertension; pre-eclampsia; NKB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 58; DB 8; Length 242; 100.0%; Pred. No. 0.056; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 2; SEQ ID NO 40; 127pp; English.
                             ADG34317 standard; protein; 242 AA.
                                                                                                                Neurokinin B antibody SEQ ID NO:40.
                                                                                                                                                                                                                                                                                                   30-MAY-2002; 2002US-0383802P.
                                                                                                                                                                                                                                                                        29-MAY-2003; 2003WO-US016802.
                                                                                                                                                                                                                                                                                                                               (HUMA-) HUMAN GENOME SCI INC.
                                                                                    (first entry)
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Best Local Similarity 100.
Matches 11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; ADG34298.
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                                                                                    26-FEB-2004
                                                                                                                                                                                                                                            11-DEC-2003.
                                                                                                                                                                                    Synthetic.
                                                        ADG34317;
RESULT 15
              ADG34317
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Search completed: October 14, 2005, 16:12:42 Job time : 84.5625 secs

221 AAWDDSLSEFL 231

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OM protein - protein search, using sw model

Run on:

October 14, 2005, 16:02:59; Search time 15:2969 Seconds (without alignments) 69:190 Million cell updates/sec

US-10-614-959-15 58 1 AAWDDSLSEFL 11 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

DB seq length: 0 DB seq length: 2000000000 Minimum I Maximum I Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	Ig lambda chain -	Ig lambda chain pr	_	٦	7	Ig lambda chain -	_	Ig lambda chain V-	_				Ig lambda chain -		ന	hypothetical prote				Ig lambda chain pr	protein kinase (EC	probable membrane	avy			cal	probable serine/th	outer membrane ush	ribonucleoside-dip
		ΠD	S36048	S78058	825750	LIHUMM	849571	S36047	S36046	LIHUWA	823627	823626	825752	825757	S25754	E87394	G95983	849113	B54802	S57428	D44151	S78057	OKBOB2	T08166	A53489	G84751	T18622	S41289	T30619	B55853	WMBY3L
		8	~	~	N	ч	~	~	N	-1	~	~	N	~	~	~	~	~	-	~	~	~	-	~	-	~	N	~	~	0	7
		Length		129	235	112	95	98	98	109	117	149	233	234	235	355	497	502	4367	110	112	130	397	1995	4344	210	329	423	443	842	882
æ	Query	Match	۲.	74.1	74.1	70.7	69.0	69.0	0.69	0.69	69.0	0.69	69.0	69.0	0.69	0.69	69.0	0.69	ó.	67.2	67.2	۲.	67.2	7.	7	Š.	•	65.5	•	5	65.5
		Score	43	43	43	41	40	40	40	40	40	40	40	40	40	40	40	40	40	39	39	39			39			38			38
	Result	No.	н	7	٣	4	S	9	7	80	6	10	11	12	13	14	15	16	17		19	20	21	22	23	24	25	56	27	28	53

hypothetical prote	conserved hypothet	outer membrane pro	conserved hypothet	thiamin biosynthes	probable thiamin b	probable PPE prote	hypothetical prote	CFTR protein - Afr	interferon alpha-I	interferon alpha-I	interferon alpha-I	interferon alpha-I	insertion element	probable sugar tra	hypothetical prote
C83366	T40104	AH0147	T40102	H84228	F84698	A70931	B69798	S23756	IVHOA1	IVHOA2	IVHOA3	IVHOA4	F81855	C98208	AF3078
~	~	~	N	~	N	~	~	N		-	-	-	~	~	7
166	259	371	395	476	644	655	857	1485	184	184	184	184	227	280	280
64.7	63.8	63.8	63.8	63.8	63.8	63.8	63.8	63.8	62.1	62.1	62.1	62.1	62.1	62.1	62.1
37.5	37	37	37	37	37	37	37	37	36	36	36	36	36	36	36
30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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A;Cross-references: EMBL:Z22189; NID:g312294; PIDN:CAA80199.1; PID:g312295; EMBL:Z22190 (S.Guberfanally: immunoglobilin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin P:15-91/Domain: immunoglobulin homology <IMM>
S36048
Ig lambda chain - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 01-Dec-1995 #text_change 21-Jan-2000
C;Accession: S36048; S36049
R;Williams, S.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       when the control of t
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Length 98;

Gaps ö 0; Indels 74.1%; Score 43; DB 2; 100.0%; Pred. No. 1.3; ative 0; Mismatches Query Match
Best Local Similarity 100.
Matches 8; Conservative

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90 AAWDDSLS 97 œ 1 AAWDDSLS 셤 ð

RESULT 2

"Granda chain precursor V-J region (clone mAB 67VL) - human (fragment)
Cispecies: Homo sapiens (man)
Cjoate: 19-Nov-1997 #sequence_revision 05-Dec-1997 #text_change 23-Jul-1999
CjAccession: 878058; 823723
Sipecies: No.
Sipecies: 10.
Sipecie

patient.
A;Reference number: S23716; MUID:92031262; PMID:1718404 A;Accession: S23723

A; Molecule type: mRNA A; Residues: 19-129 cHAW> A; Cross-references: EMBL:X54446 C; Superfamily: immunoglobulin V region; immunoglobulin homology C; Keywords: immunoglobulin F;1-18/Domain: signal sequence (fragment) #status predicted <SIG>

N

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Ig lambda chain precursor V region - human (fragment)
C;Species: Homo Sapiens (man)
C;Date: 05-Mar-1995 #sequence_revision 12-May-1995 #text_change 23-Jul-1999
C;Accession: 849571
R;Giachino, C.; Padovan, B.; Lanzavecchia, A.
R;Giachino, C.; Padovan, E.; Lanzavecchia, A.
R;Biachino, C.; Padovan, B.; Lanzavecchia, A.
R;Giachino, C.; Lanzavecchia, A.
R;Giachino, C.; Lanzavecchia, A.
R;Giachino, C.; Lanzavecchia, A.
R;Giachino, C.; Lan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C.Species: Homo sapiens (man)
C.Jate: 22-Nov-1993 #sequence_revision 01-Dec-1995 #text_change 21-Jan-2000
C.Jacession: S.S.G.47
R.Williams, S.C.
R.Williams, S.C.
submitted to the RMBL Data Library, April 1993
A.Reference number: S.36046
A.Accession: S.36047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ig lambda chain - human (fragment)
C;Species: Homo sapiens (man)
C;bate: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S;6046
R;Williams, S.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-95 «GIA>
A;Cross-references: EMBL:Z46625; NID:g575259; PIDN:CAA86595.1; PID:g575260
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:222188; NID:g312291; PIDN:CAA80198.1; PID:g312292 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heteroterramer; immunoglobulin F;15-91/Domain: immunoglobulin homology < IVM>
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A;Rosidues: 1-98 «WIL>-
A;Cross-references: EMBL:Z22187; NID:g312312; PIDN:CAA80197.1; PID:g312313
C;Superfamily: immunoglobulin V region; immunoglobulin homology
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Pred. No. 4.4;
1; Mismatches
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A;Reference number: 836046
A;Accession: 836046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 40;
Pred. No.
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    91 AAWDDSLDGYV 101
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76 AAWDDSLT 83
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Best Local Similarity
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A;Molecule type: DNA
A;Residues: 1-98 <WIL>
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Ig landac chain V-I region (Wem) - human

C; Species: Homo sapiens (man)

C; Accession: A25479

R; Mihaesco, E.; Roy, J.P.; Congy, N.; Peran-Rivat, L.; Mihaesco, C.

Bur. J. Blochem. 150, 340-357, 1985

A; Title: The amino acid sequence of a lambda light chain presenting abnormal physicochem A; Reference number: A25479; MUD:85257662; PMID:2410269

A; Accession: A25479

A; Molecule type: protein

A; Residues: 1-112 < AMIH

A; Cross-references: UNIPROT:P06887

A; Mote: residues 33-36 and some of the sequenced peptides were positioned by homology

C; Comment: The C region of this chain has the Mcg+ and Kern+ markers.

C; Genetics:

A; Genetics:
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C; Species: Homo sapiens (man)
C; Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C; Accession: $25750
Eur. J. Immunol. 21, 1513-1522, 1991
A; Title: V(Iambda) and J(lambda) -C(lambda) gene segments of the human immunoglobulin lam A; Reference number: $16439; MUID:91257162; PMID:1904362
A; Accession: $25750
A; Accession:
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F;19-129/Product: Ig lambda chain (fragment) #status predicted <MAT>F;33-109/Domain: immunoglobulin homology <IMM>
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3.3;
                                                                                                                                            DB 2;
1.7;
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100.0%; Pred. No. ...
0; Mismatches
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2; Mismatches
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Best Local Similarity 100.0
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Best Local Similarity 63.6°
Matches 7; Conservative
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Best Local Similarity 100.
Matches 8; Conservative
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C,Accession: $25752
R;Ccmbriato, G; Klobeck, H.G.
R:Ccmbriato, G; Klobeck, H.G.
Bur. J. Immunol. 21, 1513-1522, 1991
A;Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lam A;Reference number: $16439; MUID:91257162; PMID:1904362
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R;Combriato, G.; Klobeck, H.G.
Bur. J. Immunol. 21, 1513-1522, 1991
A;Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lam A;Reference number: S16439; MUID:91257162; PMID:1904362
A;Accession: S25757
                                                                                                                                                                                                             C;Species: Homo sapiens (man)
C;Accession: 19-5 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
C;Date: 13-Jan-1995 #sequence_revision 15-Jan-2000
C;Aptecestion: 831-842, 1992
A;Attle: Genetic analysis of self-associating immunoglobulin G rheumatoid factors from the A;Accession: $23623; MUID:92156804; PMID:1740665
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C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
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C,Species: Homo sapiens (man)
C,Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
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Pred. No. 6.9;
1; Mismatches
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87.5%; Pred. No. 11;
vative 1; Mismatches
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109 AAWDDSLN 116
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Best Local Similarity
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[Species: Homo sapiens (man)

[C;Species: Homo sapiens (man)

[S;Takahashi, Y.; Takahashi, N.; Tetaert, D.; Putnam, F.W.

[S;Gereace number: A01967; MUID:83221661; PMID:6407018

[S;Genetics: A;Genetics: UNIPROT:P04208

[C;Genetics: A;Genetics: A;Geneti
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C;Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C;Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C;Accession: $23627
R;Olec, T.; Lu, Ew. Huang, D.F.; Soto-Gil, R.W.; Deftos, M.; Kozin, F.; Carson, D.A.;
J. Exp. Med. 175, 831-842, 1992
A;Title: Genetic analysis of self-associating immunoglobulin G rheumatoid factors from the Reference number: $23623; MUD:92156804; PMID:1740665
A;Accession: $23627
A;Status: preliminary
A;Noslecule type: DNA
A;Residues: 1-117 < CLE>
A;Cross-references: EMBL:X59707; NID:g34426; PIDN:CAA42228.1; PID:g34427
C;Genetics:
A;Introns: 16/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-110/Domain: immunoglobulin homology < IMM>
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                                                                   DB 2; Length 98;
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                                                                Score 40; DB 2
Pred. No. 4.4;
1; Mismatches
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Pred. No.
   C; Keywords: heterotetramer; immunoglobulin
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823627
Ig lambda chain precursor - human
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                                                                   69.0%;
87.5%;
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Best Local Similarity 87.5-
                                                            Query Match
Best Local Similarity 87.5
Matches 7; Conservative
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nes 8; Conservative
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90 AAWDDSLN 97
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1 AAWDDSLS 8

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probable glycerol kinase (EC 2.7.1.30) [imported] - Sinorhizobium meliloti (strain 1021) (Species: Sinorhizobium meliloti (c;Species: National C;Species: Na
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A,Residues: 1-497 cKURA
A,Residues: 1-497 cKURA
A,Cross-references: UNIPROT:086033; GB:AL591985; PIDN:CAC49535.1; PID:g15141022; GSPDB:C
A;Cross-references: UNIPROT:086033; GB:AL591985; PIDN:CAC49535.1; PID:g15141022; GSPDB:C
B,Sabibert, F.; Finan, T.M.; Long, S.R.; Puller, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
Pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F..,
Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
A;Authors: Andenbol, M.; Vorholter; F.J.; Wells, D.H.; Wong, K.; Yeh, K.
A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Reference number: A96039; MUID:21368234; PMID:11474104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Search completed: October 14, 2005, 16:23:41
Job time : 16.2969 secs
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C, Keywords: phosphotransferase
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C;Species: Homo sapients (man)
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Date: 22-Nov-1993
R;Combriato, G; Klobeck, H.G.
Eur. J. Ishals 1522, 1991
A;Title: V(Lambda) and J(lambda) -C(lambda) gene segments of the human immunoglobulin lam A;Reference number: S16439; MUID:91257162; PMID:1904362
A;Reference number: S16439; MUID:91257162; PMID:1904362
A;Reference number: S16439; MUID:91257162; PMID:1904362
A;Reference number: S16439; MUID:913777; PIDN:CAA40956.1; PID:933738
A;Residues: 1-235 < COM>
A;Residues: 1-235 < COM>
A;Cross-references: ENMEL:XS7819; NID:933737; PIDN:CAA40956.1; PID:933738
C;Superfamily: immunoglobulin y region; immunoglobulin homology
C;Reywords: heterotetramer; immunoglobulin
F;150-218/Domain: immunoglobulin homology < IMM>
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C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Accession: E87394
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
N.J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUD:21173698; PMID:11259647
A;Status: preliminary
A;Status: DNA
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A;Cross-references: UNIPROT:Q9A925; GB:AE005673; NID:g13422491; PIDN:AAK23153.1; GSPDB:C
C;Genetics:
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                                   A;Cross-references: EMBL:X57822; NID:g33743; PIDN:CAA40959.1; PID:g33744 (S.Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin P;149-217/Domain: immunoglobulin homology <IMM>
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1; Mismatches 0; Indels
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1; Mismatches
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Similarity 87.5%;
7; Conservative
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Best Local Similarity 87.5%;
Matches 7; Conservative
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138 SAWDDSLS 145
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A;Residues: 1-234 <COM>
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RESULT 15

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Gaps

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Length 497; Indels

Score 40; DB 2; Pred. No. 26; 1; Mismatches

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homo sapien
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Q723M1
Q98W0B5
Q6C0Z1
Q74B13
Q77KB3
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SEQUENCE
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               Straubberg R.L., Feingel E.A., Grouse L.H., Derge J.G.,
Nauener R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Appkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
Biatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Brownstein M., Soares M.B., Bonaldo M.F., Carannor P.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Tochhyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McKernan K.J., Malek J.A., Gunzarte P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Wuzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,
Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
T. "Generation and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Similar to spl09HFCG Yarrowia lipolytica Calnexin.
ORFNames=KLLAOF00462g;
Kluyveromyces lactis NRRL Y-1140.
Eukaryota; Fungl; Ascomycota; Saccharomycetine; Saccharomycetes;
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Strausberg R.;
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC030984; AAH30984.1; -.
HSSP; P01703, 7FAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11 procein. - - - 236 AA; 25024 MW; 1703B77942630E08 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS50835; IG LIKE; 2.
PROSITE; PS00290; IG MHC; UNKNOWN 1.
Hypothetical protein.
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InterPro; IPR003597; Ig_c1.
InterPro; IPR003006; Ig_WHC.
InterPro; IPR003596; Ig_W.
Pfam; PP07654; C1-8et; 1.
SWART; SM00406; IGV; 1...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and mouse cDNA sequences."
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STRAIN=NRRL Y-1140;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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Q6CLT9
DDT TO DD
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-!- MISCELLANEOUS: Residues 33-36 and some of the sequenced peptides
were positioned by howology.
-!- MISCELLANEOUS: The C region of this chain has the Mcg+ and Kern+
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Mihaesco E., Roy J.P., Congy N., Peran-Rivat L., Mihaesco C.;
"The amino acid sequence of a lambda light chain presenting abnormal
physicochemical and antigenic features.";
Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O., Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A., Swennene D., Tekaia P., Wesolowski-Louvel M., Westhof E., Wirth B., Eaniou-Meyer M., Zivanovic I., Bolotin-Pukuhara M., Thierry A., Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J. Wincker P., Soudiet J.L., "Genome evolution in yeasts.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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InterPro; IPkuv...
Pfam; PP00047; ig; 1.
SMART; SM00406; IGY; 1.
PROSITE; PS50815; IG_LIKE; 1.
Pirect protein sequencing; Immunoglobulin V region;
Monoclonal antibody; Pyrrolidone carboxylic acid.
nOMAIN
1 106
Pyrrolidone carboxylic acid.
nOMAIN
1 106
By similarity.
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                                                                                                                                                                                                                                                                                                                                                             Genoscope;
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; CR381216; CAG97807.1; -.
GO; GO:0005514; F:calcium ion storage activity; IEA.
InterPro; IPR001580; Calret/Calnex.
InterPro; IPR008985; Cond like_lec_g1.
Pfam; PF00526; Calreticulin; 1.
PRINTS; PR00626; Calreticulin; 1.
PROSITE; PS00803; CALRETICULIN .
PROSITE; PS00803; CALRETICULIN 1.
PROSITE; PS00805; CALRETICULIN 1.
PROSITE; PS00805; CALRETICULIN 1.
SEQUENCE 628 AA; 70981 MW; B0DBA6D1A64644EE CRC64;
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HSSP, PO1703; PRAB.
GO; GO:000576; C:extracellular; NAS.
GO; GO:0005825; F:antigen binding; NAS.
GO; GO:0006955; F:immune response; NAS.
InterPro; IPR007110; IG-like.
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01-07NV-1988 (Rel. 06, Last sequence update)
05-0UL-2004 (Rel. 44, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 66.7 ses 6; Conservative
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P06887;
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109 AAWDDSMS 116
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P04208;
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SEQUENCE
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Q9A925,
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LV1F HUMAN
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Matches
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A Klausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
A Klausher R.D., Collins F.S., Wagner L., Schaefer C.R., Bhat N.K.,
Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McKennan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Rachards S., Wolley K.C., Hale S., Garcherko Y., Bouffard G.G.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Jones S.J., Marra M.A.,
Jones M. J. Jones S.J., Marra M.A.,
Jones S.J., Marra M.J.,
Jones S.J., Marra M.J.,
Jor
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                     Score 41; DB 1; Length 112;
Pred. No. 12;
                                                                                                                 2; Indels
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Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
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237 AA; 25108 MW; 6814170F7B784825 CRC64;
     112 AA; 11789 MW; 748124F079CFFBE4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                237 AA
                                                                                                                 2; Mismatches
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InterPro; IPR003599; Ig.
InterPro; IPR003599; Ig.
InterPro; IPR003599; Ig.
InterPro; IPR003599; Ig.
InterPro; IPR003596; Ig.MHC.
InterPro; IPR003596; Ig.W.
Pfam; PF070644; C1-set; I.
Pfam; PF00047; Ig. 2.
SWART; SW00409; IG; 2.
SWART; SW00406; IG.Y.
PROSITE; PS50835; IG.LIKE; 2.
PROSITE; PS50835; IG.LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
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                                                     h 70.7%;
Similarity 63.6%;
7; Conservative
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                                                                                                                                                                                                                 91 AAWDDSLDGYV 101
                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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TISSUE-Primary B-Cells;
                                                                                                                                                                          1 AAWDDSLSEFL 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Primary B-Cells;
                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
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SECUENCE.

MEDLINE=8321661; PubMed=6407018;
Takahashi X., Takahashi N., Tetaert D., Putnam F.W.;
Takahashi X., Takahashi N., Tetaert D., Putnam F.W.;
"Complete covalent structure of a human immunoglobulin D: sequence of the lambda light chain.";
Proc. Natl. Acad. Sci. U.S.A. 80:3686-3690(1983).
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STRAIN=ATCC 19089 / CB15;

MEDLINE=2113698; PubMed=11259647; DOI=10.1073/pnas.061029298;

MEDLINE=21136998; PubMed=11259647; DOI=10.1073/pnas.061029298;

Mierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,

Bisen J.A., Heldelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,

Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.

DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,

Kolonay J.F., Smit J., Craven M.B., Khouri H.M., Shetty J.,

Berry K.J., Utterback T.R., Tran K., Wolf A.M., Vamathevan J.J.,

Ermolaeva M.D., White O., Salzberg S.L., Venter J.C., Shapiro L.,
                                                                                                                                      Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales; Caulobacteraceae; Caulobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 40; DB 1; Length 109;
Pred. No. 18;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         109 AA; 11725 MW; B17785F6A8DF9BAC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct protein sequencing; Immunoglobulin V region. DOMAIN 1 97 V sequent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein CC1169.
OrderedLocusNames=CC1169;
                                         20-WAR-1987 (Rel. 04, Created)
20-WAR-1987 (Rel. 04, Last sequence update)
20-UIL-2004 (Rel. 44, Last annotation update)
Ig lambda chain V-I region WAH.
109 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        355 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP, P01703, 7FAB.

GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; IG-like.
InterPro; IPR03596; Ig_v.
Ffam; PF00047; ig; 1.
FMART; SMO0406; IGy; 1.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J segment
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 80.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       109
89
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90 AAWDDSLWVF
                                                                                                                                                                                                           NCBI_TaxID=9606;
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IIGR;

SKRRAGRARAS

Matches

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SECUENCE FROM N.A. (ISOFORM 1).
MEDLINE=20304757; PubMed=10843809; DOI=10.1006/geno.2000.6179;
Jenne D.E., Tinschert S., Stegmann E., Reimann H., Nurnberg P.,
HORN D., Naumann I., Buske A., Thiel G.;
"A common set of at least 11 functional genes is lost in the majority of NF1 patients with gross deletions.";
Genomics 66:93-97(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-Leukocyte;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshlyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORM 1).
MEDILINE-2201451; PubMed=12018930;
Whitley P., Gibbard A.M., Koumanov F., Oldfield S., Kilgour B.E.,
Prestwich G.D., Holman G.D.;
"Identification of centaurin-alpha2: a phosphatidylinositide-binding
protein present in fat, heart and skeletal muscle.";
Bur. J. Cell Biol. 81:222-230 (2002).
                                                                                                                                                                                                                                                                  PH 2.
R->C: Almost complete loss of InsP4
binding.
R->C: No loss of InsP4 binding, Almost
complete loss of InsP4 binding; when
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
Pfam; PF01412; ArfGap; 1.
Pfam; PF0169; PH; 2.
PRINTS; PR00405; REVINTRACTNG.
SMART; SM00105; ArfGap; 1.
SMART; SM00233; PH; 2.
PROSITE; PS500115; ARFGAP; 1.
PROSITE; PS50003; PH_DOMAIN; 2.
DOMAIN
9 130 Arf-GAP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 40; DB 1; Length 376;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [3]
SEQUENCE FROM N.A. (ISOFORM 1).
Bertsch U., Illies C., Mayr G.W.;
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                   376 AA; 43524 MW; E357392F38F07166 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                          associated with C-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        O9NPF8; Q8N406; Q96SD5;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                               69.0%; Scor.
66.7%; Pred. No. b.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         381 AA.
                                                                                                                                                                                                                       C4-type.
PH 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best_Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                            151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69 WDDSMVEFM 77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                            275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=CENTA2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                       ZN FING
                                                                                                                                                                                                                                                                                            MUTAGEN
                                                                                                                                                                                                                                                                                                                                            MUTAGEN
                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                       DOMAIN
     DAR WILL TITIES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-22012451; PubMed=12018390;

Mitlay P., Gibbard A.M., Koumanov F., Oldfield S., Kilgour E.B.,

Prestavich G.D., Holman G.D.;

Mitlay P., Gibbard A.M., Koumanov F., Oldfield S., Kilgour E.B.,

Protein present in fat, heart and skeletal muscle.";

Bur J. Cell Biol. 81:22-220 (2002).

L. SUNCTION: GTPase-activating protein for the ADP ribosylation

factor family (Potential).

-1- STBUNIT: Binds phosphatidylinositol 4,5-bisphosphate.

-1- STBUNIT: Binds phosphate (InsP4). Binding of phosphatidylinositol

1,3,4,5-tetrakisphosphate (InsP4). Binding of phosphatidylinositol

1,3,4,5-tetrakisphosphate (InsP4). Binding of phosphatidylinositol

2,5-bisphosphate and phosphatidylinositol 3,4-bisphosphate occurs

at a much lower affinity. Possesses a stoichiometry of two binding

SIES for InsP4 with identical affinity (By similarity).

-1- SUBCELLULAR LOCATION: Cytoplasmic. Constitutively associated with

the plasma membrane. Excluded from the nucleus (By similarity).

-1- TISSUE SPECIFICITY: Expressed in many tissues, with highest levels

in fat, heart and skeletal muscle. Also detected in kidney, liver
                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., INTERACTION WITH PTDINS(4,5)P2, PTDINS(3,4,5)P3 AND INS(1,3,4,5)P4, TISSUE SPECIFICITY, AND MUTAGENESIS OF ARG-151 AND
                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus (Rat).
Bukaryota, Metaroa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                     Length 355;
                                                                                                                                                                                                                                                                                                                   Indels
                    "Complete genome sequence of Caulobacter crescentus.";
Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
EMBL; AE005795; AAK23153.1; -.
PIR; E87394; E87394.
                                                                                                                                      InterPro; IPR011251; Luciferase like.
Pfam; PP00296; Bac luciferase; I.
Complete proteome; Hypothetical protein.
SEQUENCE 355 AA; 38552 MW; 3C4AEF428255557 CRC64;
                                                                                                                                                                                                                                                                  69.0%; Score 40; DB 2;
87.5%; Pred. No. 63;
cive 1; Mismatches (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-OCT-2004 (Rel. 45, Created)
25-OCT-2004 (Rel. 45, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        376 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SIMILARITY: Contains 1 Arf-GAP domain.
-!- SIMILARITY: Contains 2 PH domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (Se
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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InterPro; IPR001164; hRIP_like.
InterPro; IPR001849; PH.
InterPro; IPR011036; PH_related.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AJ238993; CAB88403.1; -.
                                                                                                                                                                                                                                                                                                                   7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                              138 SAWDDSLS 145
                                                                                                                                                                                                                                                                                                                                                                   1 AAWDDSLS 8
                                                                                                                                                                                                                                                                                            Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Centaurin alpha 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Adipocyte;
                                                                                                                    CC1169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CEA2 RAT
                                                                                                                                                                                                                                                                     Query Match
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Gaps

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1; Indels

**29JK15** 

RESULT

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Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lux K., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A., "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IsoId=Q9NPF8-2; Sequence=VSP_011180; Note=May be due to a competing acceptor splice site. No experimental confirmation available; TISSUE SPECIFICITY: Highly expressed in placenta, spleen, kidney, selecteal muscle and adrenal gland. Weakly expressed in Infyroid, liver, heart, lung, small intestine, peripheral blood leukocytes. Not detected in spinal cord, brain, stomach, trachea, colon, lymph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ractor raming (Forential).
SUBUNIT: Binds phosphatidylinositol 3,4,5-trisphosphate (PtdInsP3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: Cytoplasmic. Constitutively associated with the plasma membrane. Excluded from the nucleus.
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS50115; ARFGAP; 1.
PROSITE; PS50003; PH DOMAIN; 2.
Alternative splicing; GTPase activation; Metal-binding; Repeat; Zinc;
Zinc-finger.
                                                                                                                                                                                                                                                                                                                                            Hanck T., Stricker R., Sedehizade F., Reiser G.; Indentification of gene structure and subcellular localization of human centaurin alpha 2, and p421P4, a family of two highly homologous, Ins 1,3,4,5-P4-/PtdIns 3,4,5-P3-binding, adapter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- FUNCTION: GTPage-activating protein for the ADP ribosylation
factor family (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and inositol 1,3,4,5-tetrakisphosphate (InsP4). Possesses a stoichiometry of two binding sites for InsP4 with identical
                                                                                                                                                                                                                                                                                  INTERACTION WITH PTDINS(3,4,5)P3 AND INS(1,3,4,5)P4, TISSUE SPECIFICITY, AND SUBCELLULAR LOCATION.
PubMed=14690521;
                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: Contains 1 Arf-GAP domain. SIMILARITY: Contains 2 PH domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IsoId=Q9NPF8-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Interpro; IPR001164; hRIP_like.
Interpro; IPR001849; PH.
Interpro; IPR011036; PH related.
Pfam; PP01412; ArfGap; I.
Pfam; PP0169; PH; 2.
PRINTS; PR00405; REVINTRACTNG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AJ238994; CAB88383.1; -. EMBL; AJ272195; CAB77266.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         J. Neurochem. 88:326-336(2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAC40651.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; BC033758; AAH33758.1; -.
                                                                                                                                                                                                                        and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HGNC:16487; CENTA2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00105; ArfGap; 1.
SMART; SM00233; PH; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   node and bone marrow.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    H-InvDB; HIX0013699; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AJ242782;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           affinity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MIM; 608635;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=1
                                                                                                                                                                                                                                                                                                                                                                                                                                     proteins."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL;
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STRAIN=FVB/N; TISSUE=Breast tumor;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Klausner R.D., Collins F.S., Magner L. Shenmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Heigh F.,

A Diatchenko L., Marusina K., Parmer A.A., Rubin G.M., Heigh F.,

B Diatchenko L., Marusina K., Parmer A.A., Rubin G.M., Heigh F.,

A Diatchenko L., Marusina K., Parmer A.A., Rubin G.M., Hang L.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninoi P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

B Boak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Willalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

A Milting M., Touchman J.W., Green E.D., Dickson M.C.,

B Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

B Butterfield Y.S.N., Krzywniski M.I., Skalska U., Smailus D.E.,

B Cherration and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proc. Natl. Acad. 2011. U.S.A. 99:16899-16903 (2002).

-! FUNCTION: GTPage-activating protein for the ADP ribosylation factor family (Potential).

-! SUBUNIT: Binds phosphatidylinositol 3,4,5-trisphosphate (PtdInsP3) and inositol 1,3,4,5-tetrakisphosphate (InsP4). Possesses a stoichiometry of two binding sites for InsP4 with identical affinity (By similarity).

-! SUBCELLUIAR LOCATION: Cytoplasmic. Constitutively associated with the plasma membrane. Excluded from the nucleus (By similarity).

-! SIMILARITY: Contains 1 Aff-GAP domain.
                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      us muscurus (mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                               ö
                                                                                                                                                                                  69.0%; Score 40; DB 1; Length 381; 66.7%; Pred. No. 68; 1; Indels ive 2; Mismatches 1; Indels
Arf-GAP.

C4-type.
PH 1.
PH 2.
Missing (in isoform 2).
/FTIG4VSP 011180.
i. > P (in Ref. 3).
i. > P (in Ref. 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-0CT-2004 (Rel. 45, Created)
25-0CT-2004 (Rel. 45, Last sequence update)
25-0CT-2004 (Rel. 45, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                 381 AA
                                                                                                                                                381 AA; 44348 MW;
                                                                                                                                                                                                       66.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and mouse cDNA sequences."
                                                                                                                                                                                                                               6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                     3 WDDSLSEFL 11
                                                                                                                                                                                                                                                                                                           69 WDDSIVEFM 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse)
                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Centaurin alpha 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
      25
132
255
269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=Centa2;
                                                                                                                                                                                                                                                                                                                                                                                                               CEA2 MOUSE
Q8R2V5;
                                                               DOMAIN
VARSPLIC
                                                                                                                                                SEQUENCE
    DOMAIN
ZN FING
DOMAIN
                                                                                                                         CONFLICT
                                                                                                                                                                                                                             Matches
      SOTETTE
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
There are no restrictions on
                                                                                                                          EMBL; AL591985; CAC49535.1; -.

EMBL; AR680548; AAD12735.1; -.

EMBL; AP680548; AAD12735.1; -.

EMBL; AP680548; AAD12735.1; -.

HSPP; P08859; IGLC.

HAMAP; MF 00186; -; 1.

InterPro; IPR001057; FGGY kin.

InterPro; IPR00599; GIycerol_kin.

Pfam; PF00370; FGGY_N; 1.

Pfam; PF00370; FGGY_N; 1.

PROSITE; PS00933; FGGY_KINASES_1; FALSE_NEG.

PROSITE; PS00445; FGGY_KINASES_2; 1.

ATP-binding; Complete proteome; Glycerol metabolism; Kinase; Plasmid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69.0%; Score 40; DB 2; Length 502; 60.0%; Pred. No. 91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 497;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=HUB 5-2-4;
Juerchott K., Boerner T.;
Juerchott K., Boerner T.;
Juerchott K., Boerner T.;
Submitted (NOV-1993) to the EMBL/GenBank/DDBJ databases.
EMBL; Z2837; CAR82191-1; -.
PIR; S49113; S49113.
InterPro; IPR000345; CytC_heme_BS.
InterPro; IPR000345; VirE.
PEAM; PF05272; VirE.
PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
SEQUENCE 502 AA; 58859 MW; 98E6ID5CZ14520E6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                       153 165 ATP (Probable).
497 AA; 54419 MW; 42D3428335ACC2B7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Microcystis aeruginosa.
Bacteria; Cyanobacteria; Chroococcales; Microcystis.
NCBI_TaxID=1126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69.0%; Score 40; DB 1; 70.0%; Pred. No. 90; tive 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-FEB-2003 (Rel. 32, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
25-GCT-2004 (Rel. 45, Last annotation update)
Putative helicase C28H8.3 (EC 3.6.1.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          502 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Mismatches
  European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 70.0 nes 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             197 AWDDELTEVL 206
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434 SWEDELAEFL 443
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 13
YP93_CAEEL
ID YP93_CAEEL
AC 009475;
                                                                                                                                                                                                                                                                                                                                                                                                                       Transferase
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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Q48904;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDILINE-21396508; PubMed=11481431; DOI=10.1073/pnas.161294698; Finan T.M., Weidner S., Wong K., Buhrmester J., Chain P., Vorhoelter F.J., Hernandez-Lucas I., Becker A., Cowie A., Gouzy J., Golding B., Puehler A.; 
Glding B., Puehler A.; 
fixing endosymbiont sinorhizobium meliloti."; 
Proc. Natl. Acad. Sci. U.S.A. 98:9889-9894(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=SU47 / 1021,
MEDILINE=99121023; PubMed=9922248;
MEDILINE=99121023; PubMed=9922248;
MEDILINE=99121023; PubMed=9922248;
MEDILINE=99121023; PubMed=9922248;
MEDILINE=99121023; PubMed=9022248;
MEDILINE=99121023; PubMed=9022248;
MEDILINE=99121023; MEDILINE=99122248;
MEDILINE=99121023; MEDILINE=99122248;
MEDILINE=99121023; MEDILINE=99122248;
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MEDILINE=99121023; MEDILINE=99122248;
MEDILINE=99121023; MEDILINE=99122248;
MEDILINE=99122248;
MEDILINE=991212023; MEDILINE=99122248;
MEDILINE=99122448;
MEDILINE=99122448;
MEDILINE=99122448;
MEDILINE=99122448;
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MEDILINE=99124484;
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MEDILINE=9912448448;
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MEDILINE=9912448448;
MEDILINE=99124484848;
MEDILINE=99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ocyvery 2000 (Rel. 39, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Glycerol kinase (EC 2.7.1.30) (ATP:glycerol 3-phosphotransferase)
(Glycerokinase) (GK).
Name=glpK; OrderedLocusNames=RB1135; ORFNames=SMb21009;
Name=glpK; OrderedLocusNames=RB1135; ORFNames=SMb21009;
Phizoblum mellioti (Sinorhizobium mellioti).
Plasmid pSymB (megaplasmid 2).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizoblacese; Sinorhizobium/Ensifer group; Sinorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     metabolism.
-!- CATALYTIC ACTIVITY: ATP + glycerol = ADP + sn-glycerol 3-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          phosphate.
--- PATHWAY: Glycerol utilization; rate-limiting step.
--- SIMILARITY: Belongs to the fucokinase / gluconokinase / glycerokinase / xylulokinase family.
                                                                                                                                                                                                                          SMART; SM00233; Fu; ...
PROSITE; PSS0115; ARFGAP; 1.
PROSITE; PSS0003; PH DOMAIN; 2.
GTPase activation; Metal-binding; Repeat; Zinc; Zinc-finger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 40; DB 1; Length 381;
Pred. No. 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                     2E504CEF0ACD84D5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              497 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Mismatches
                                                                                                                                                                                                                                                                                                                                    C4-type.
PH 1.
                                           MGD; MGI:2663075; Centa2.
InterPro; IPR001164; hRIP_like.
InterPro; IPR001164; PH.
InterPro; IPR0011036; PH related.
Pfam; PF001412; ArfGap; I.
Pfam; PR00169; PH; 2.
PRINTS; PR00405; REVINTRACTNG.
SMART; SM00105; ArfGap; 1.
                           EMBL; BC027165; AAH27165.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                     43989 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                            69.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 1-59 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 WDDSLSEFL 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 69 WDDSMVEFM 77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=382;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GLPK RHIME
086033;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=1021;
                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                DOMAIN
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GLPK_RHIME
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Gaps

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Gaps

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DOMAIN
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ORFNames=C28H8.3;
Caenorhabditis elegans.
Bukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=74-0R23-1A / FGSC 987,
MEDLINE=95014704; PubMed=7929559; DOI=10.1083/jcb.127.1.139;
Plamann M., Minke P.F., Tinsley J.H., Bruno K.S.;
"Cytoplasmic dynein and actin-related protein Arp1 are required for
                                                                                                                                                                                                                                                                                                    Waterston R.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
-1- SUBCELLULAR LOCATION: Nuclear (Potential).
-1- SIMILARITY: Belongs to the helicase family. SKI2 subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                         STRAIN=Bristol N2;
MEDLINE=99069613; PubMed=9851916;
The C. elegans sequencing consortium;
"Genome sequence of the nematode C. elegans: a platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 40; DB 1; Length 1714; Pred. No. 3.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1714 AA; 194095 MW; 0936764D27C7EFAD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001410; DEAD.
InterPro; IPR001410; DEAD.
InterPro; IPR001450; Helicase_C.
Pfam; PF00270; DEAD; 1.
SMART; SM00487; DEXDc; 1.
SMART; SM00487; DEXDc; 1.
TIGRPAMS; TIGR0180; Cas TM1810; 2.
ATP-binding; Helicase; Hydrolase; Hypothetical protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Potential).
(Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DYHC_NEUCR STANDARD; PRT; 4367 AA. P45443; QTNVH1; 12.00V-1995 (Rel. 32, Created) 01-NOV-1995 (Rel. 32, Last sequence update) 05-JUL-2004 (Rel. 44, Last annotation update) 105-JUL-2004 (Rel. 44, Last annotation update) Nume=ro-1; ORFNames=NCU06976.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATP (Poten
ATP (Poten
DEVH box.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U20861; AAA62291.2; -.
WormBase; WBGene00016194; C28H8.3.
WormPep; C28H8.3; CE29195.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88.98;
                                                                                                                                                                                                                          investigating biology.";
Science 282:2012-2018(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8; Conservative
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813
916
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Best Local Similarity
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                                                                                                                      SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=5141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nuclear protein.
                                                                                NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                    REVISIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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BIND
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DYHC NEUCR
1D DYHC N
AC P45431
DT 01-NOV
DT 01-NOV
DT 05-JUL
DB DYMEIN
GN Nemein
GN Nemein
GN Neuroß
OC Bukary
OC Bukary
OC SCORT
KR [1]
RR [1]
RR SEDURN
RC STRAIN
RX MEDLIN
RA MEDLIN
RA
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PROBLEME FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SETAIN=14-0523-1A, FOSC 987;

RAMAN=1-0523-1A, FOSC 987;

RAMAN=1-051-10.1038/nature01554;

RAMEG=12712197; DOI=10.1038/nature01554;

RAMEG=12712197; DOI=10.1038/nature01554;

RAMEG=1.C., Ramed N., Ma L.-J., Smirnow S., Putterel S., Rehman B.,

RAMEGE D., Flatzheny W., Ma L.-D., Nelson M.A.,

RAMEGH S., Schulte U., Kothe G.O., Jedd G., Mewes H.-W., Staben C.,

RAMEGH S., Greenberg D., ROA, * Follow M.A.,

RAMEGH S., Greenberg D., ROA, * Follow D., Kramey M.A.,

RAMEGH S., Belake C., Rudd S., Frishman D., Krystofowa S.,

RAMEGH S., Matzenberg R., Greenberg R., Gnerre S., Kamal M., Kamvysselis M.,

RAMEGH S., Metzenberg D., Li W., Pratt R.J., Opmani S., Cogoni C.,

RAMEGH S., Mannhaupt G., Bibble D.J., Frishray S.,

RAMEGH S., Mannhaupt G., Bibble D.J., Frishray M.,

RAMEGH S., Alex L., Mannhaupt G., Bibble D.J., Frishray M.,

RAMEGH S., Londer B.S., Lander E.S., Nusbaum C., Birren B.,

RAUTH Genome sequence of the filamentous fungus Neurospora crassa.";

RAUTH Genome sequence of the filamentous fungus Neurospora crassa.";

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RAUTH Genome sequence of the filamentous fungus Neurospora crassa.";

RAUTH Genome sequence of the filamentous fungus neuroker stemple of thought to occur on release of ADP. Required to maintain uniform nuclear distribution in hyphae.

C. SUBGELULAR LOCATION: Cytoplasmic.

-1-SUBGILLAR LOCATION: Cytoplasmic.

-1-SUBGILLAR LOCATION: Cytoplasmic.

-1-SUBGILLAR LOCATION: Cytoplasmic.

-1-DOMAIN: Dynein heavy chains probably consist of an N-terminal stem (which binds cargo and interacts with other dynem at 130, and the head or motor domain. The motor contains six tandemly site. A seventh domain 
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1904 AAA 1 (By similarity).

2460 AAA 2 (By similarity).

2815 AAA 3 (By similarity).

2816 AAA 3 (By similarity).

3179 AAA 4 (By similarity).

3179 AAA 6 (By similarity).

4215 AAA 6 (By similarity).

4215 AAA 6 (By similarity).

693 Coiled coil (Potential).

1215 Coiled coil (Potential).

1574 Coiled coil (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: Belongs to the dynein heavy chain family.
mal nuclear distribution in filamentous fungi."; Cell Biol. 127:139-149(1994).
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InterPro; IPR004273; Dynein_heavy.
Edm; PP03028; Dynein_heavy; 1.
SWART; SW00382; AAA; 3.
ATP-binding; Coiled coil; Dynein; M
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2; Mismatches 1; Indels
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Vibrionaceae, Vibrio.
NCBI_TaxID=670;
2218 Coiled coil (Potential).
2218 Coiled coil (Potential).
3296 Coiled coil (Potential).
3481 Coiled coil (Potential).
3809 ATP (Potential).
2247 ATP (Potential).
2612 ATP (Potential).
265568 MW, 1B10F3B2D170bGDF CRC64;
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein VPA1212.
OrderedLocusNames=VPA1212;
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                                                                                                                                          October 14, 2005, 16:00:04; Search time 21.6562 Seconds (without alignments) 37.917 Million cell updates/sec
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Copyright (c) 1993 - 2005 Compugen Ltd.
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RESULT 4
US-08-350-260A-374
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Sequence 15, Application US/08652816A

Patent No. 587215

GENERAL INFORMATION:

APPLICANT: Obsourn, JK

APPLICANT: Allen, DJ

APPLICANT: McGefferty, JG

TITLE OF INVENTION: Specific binding members, materials and
TITLE OF INVENTION: Details 53

CORRESPONDENCE ADDRESS:

NUMBER OF SEQUENCES: 53

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 South Wacker Drive CITY: Chicago

STATE: Illinois

COUNTRY: United States of America

COMPUTRY: United States of America

COMPUTRY: In EMP Compatible

COMPUTRY: BEND COMPATION

SOFTWARE PETAING SYSTEM: PC-DOS/MS-DOS

SOFTWARE PETAING NUMBER: US/08/652,816A

FILING APPLICATION NUMBER: US/08/652,816A

FILING APPLICATION NUMBER: GB 9125579.4

FILING APPLICATION NUMBER: GB 9125579.4
                 The Isolation and Production of Catalytic Antibodies using Phage Technology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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TITLE OF INVENTION: The Isolation and Production of TITLE OF INVENTION: Catalytic Antibodies using Phage NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS: ADDRESSE: ADDRESSE: IGEN INC.
STREET: 1530 East Jefferson St.
CITY: ROCKVILLE
CONTRY: USA
ZIP: 20852
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9125579.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 63: SEQUENCE CHARACTERISTICS: LENGTH: 104 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 104 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , MOLECULE TYPE: protein US-08-273-146-63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 AAWDDSLSEFL 11
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PRILLORY APPLICATION NATE: 0205118.9

PRILOR APPLICATION NATE: 0205118.9

PRILOR APPLICATION NATE: 024-084.192

PRILOR APPLICATION NATE: 024-084.192

PRILOR APPLICATION NATE: 025-1932

PRILOR APPLICATION NATE: 025-1932

PRILOR APPLICATION NATE: 025-1932

PRILOR APPLICATION NATE: 026-1932

PRILOR APPLICATION NATE: 026-1934

PRILOR APPLICATION NATE: 026-1934
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APPLICANT: Winter, Gregory Paul
APPLICANT: Griffiths, Andrew David
APPLICANT: Williams, Samuel Cameron
APPLICANT: Williams, Samuel Cameron
APPLICANT: Nissim, Ahuva
APPLICANT: Johnson, Kevin Stuart
APPLICANT: Smith, Andrew John Hammond
TITLE OF INVENTION: binding pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
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CORRESPONDENCE ADDRESS:
ADDRESSEE: David W. Clough
STREET: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                NAWE: Bartnicki, Audrey L.
REGISTATION NUMBER: 40,499
REFERENCE/DOCKET NUMBER: 28111/32372A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
INFORMATION FOR SEQ ID NO: 374:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 46; DB 4;
Pred. No. 0.05;
                                                                                   PILLING DATE: 05-DEC-1994

PILLING DATE: 15-MAY-1991

PILLING DATE: 15-MAY-1991

APPLICATION NUMBER: GB 910549.4

PILLING DATE: 15-MAY-1991

APPLICATION NUMBER: PCT/GB92/00883

FILLING DATE: 15-MAY-1992

APPLICATION NUMBER: PCT/GB93/00605

FILLING DATE: 34-MAR-1993

APPLICATION NUMBER: US 08/150,002

FILLING DATE: 31-MAR-1994

APPLICATION NUMBER: US 08/150,002

FILLING DATE: 16-SEP-1994

ATTORNEY/AGENT INFORMATION:
             APPLICATION NUMBER: US/09/104,337A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Mismatches
                                                                        APPLICATION NUMBER: US 08/350,260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLGY: linear;
; SEQUENCE DESCRIPTION: SEQ ID NO: 374:
US-09-104-337A-374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 346, Application US/08350260A; Patent No. 5962255; GENERAL INFORMATION:
                               FILING DATE: 25-Jun-1998 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 11 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             79.38;
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Best Local Similarity 72.7
Matches 8; Conservative
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STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-350-260A-346
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Johnson, Kevin Stuart
Smith, Andrew John Hammond
TITLE OF INVENTION: Methods for producing members of specific
binding pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Andrey L. Bartnicki
STREET: Marshall, Gerstein & Borun
6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 46; DB 2; Length 11;
Pred. No. 0.05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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CONTRX: USA
CONTRX: USA
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS_DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REPERENCE/DOCKET NUMBER: 2011/32372
TELECOMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
INFORMATION FOR SEQ ID NO: 374:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acide
TYPE: amino acid
STRANDEDNESS: single
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 15-MAY-1991
PRIOR APPLICATION NUMBER: GB 9110549.4
FILING DATE: 15-MAY-1991
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
PRIOR APPLICATION NUMBER: PCT/GB91/01134
FILING DATE: 10-JUL-1991
PRIOR APPLICATION NUMBER: PCT/GB92/00883
APPLICATION NUMBER: PCT/GB92/00883
FILING DATE: 15-MAY-1992
PRIOR APPLICATION NUMBER: DCT/GB93/00605
FILING DATE: 34-MAR-1993
APPLICATION NUMBER: US 08/150,002
FRIDK APPLICATION DATA: 31-MAR-1994
PRIOR APPLICATION DATA: 31-MAR-1994
APPLICATION NUMBER: US 08/307,619
FRIDK DATE: 31-MAR-1994
APPLICATION NUMBER: 36,107
BEGISTRAFION NUMBER: 36,107
BEGISTRAFION NUMBER: 36,107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Griffiths, Andrew David
Williams, Samuel Cameron
Waterhouse, Peter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 374, Application US/09104337A
Patent No. 6492160
GENERAL INFORMATION:
GENERAL MAINEER, Gregory Paul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       79.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
nes 8; Conserv
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Best Local S
Matches 8
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Gaps

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Sequence 60, Application US/08665202
Patent No. 5977322
GENERAL INFORMATION:
APPLICANT: Marks, James D.
APPLICANT: Schier, Robert
TITLE OF INVENTION: Tumor Antigens
NUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,202

FILING DATE: 13-JUN-1996

CLASSIFFICATION DATA:
APPLICATION NUMBER: US 60/000,238

FILING DATE: 14-JUN-1995

FILING DATE: 14-JUN-1995

FILING DATE: 15-JUN-1995

FILING DATE: 15-JUN-1995

FILING DATE: 15-JUN-1995
                     PRIOR APPLICATION NOMBER: US/09/104,337A
FILING DATE: 25-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/350,260
FILING DATE: 15-MAY-1991
APPLICATION NUMBER: GB 9110549.4
FILING DATE: 12-MAY-1991
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
APPLICATION NUMBER: PCT/GB93/00605
FILING DATE: 15-MAY-1993
APPLICATION NUMBER: PCT/GB93/00605
FILING DATE: 31-MAR-1994
APPLICATION NUMBER: US 08/350,619
FILING DATE: 16-SEP-1994
ATTORNEY/AGBNT INFORMATION:
NAME: BATTOL AND DATE: 16-SEP-1994
ATTORNEY/AGBNT INFORMATION:
NAME: BATTOL ON NUMBER: US 08/307,619
FILING DATE: 16-SEP-1994
ATTORNEY/AGBNT INFORMATION:
NAME: BATTOL ON NUMBER: 40,499
REFERENCE/DOCKET NUMBER: 28111/32372A
TELECOMMUNICATION NUMBER: 28111/32372A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 346:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: 312-474-6300
INFORMATION FOR SEQ ID NO: 346:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 72...
Best Local 8; Conservative
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US-08-665-202-60
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Johnson, Kevin Stuart
Smith, Andrew John Hammond
TITLE OF INVENTION: Methods for producing members of specific
binding pairs
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COMPUTER: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: TBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSE: Audrey L. Bartnicki
STREBT: Marshall, Gestein & Borun
6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   75.9%; Score 44; DB 2; Length 11; 72.7%; Pred. No. 0.11; 1; Indels ive 2; Mismatches 1; Indels
                        APPLICATION NUMBER: GB 9110549.4
FILING DATE: 15-MAY-1991
RION APPLICATION DATA:
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
RION APPLICATION DATA:
APPLICATION NUMBER: PCT/GB91/01134
FILING DATE: 10-JUL-1991
RICH APPLICATION NUMBER: PCT/GB92/00683
FILING DATE: 15-MAY-1992
RICH APPLICATION DATA:
APPLICATION NUMBER: PCT/GB93/00605
FILING DATE: 15-MAY-1993
FILING APPLICATION DATA:
APPLICATION NUMBER: PCT/GB93/00605
FILING APPLICATION DATA:
APPLICATION NUMBER: PCT/GB93/00605
FILING APPLICATION DATA:
APPLICATION NUMBER: DCT/GB93/00605
FILING APPLICATION DATA: DCT/GB93/00605
FILING APPLICATION DATA: DCT/GB93/00605
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Griffiths, Andrew David
Williams, Samuel Cameron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28111/32372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 08/150,002
FILING DATE: 31-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/307,619
FILING DATE: 16-SEP-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 346, Application US/09104337A Patent No. 6492160 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Clough, David W
REGISTRATION UNDRER: 36,107
REFERENCE/DOCKET UNDRER: 28111
TELECOMMUNICATION INFORMATION:
TELEPHORE: 312-474-6300
INFORMATION FOR SEQ 1D NO: 346:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Waterhouse, Peter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 72.7
Matches 8; Conservative
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COUNTRY: USA
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linear
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US-08-350-260A-346
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TELEPHONE: 312-474-6300
INFORMATION FOR SEQ ID NO: 339:
SEQUENCE CHARACTERISTICS:
       MOLECULE TYPE: peptide
                                                                                                                                                                   1 AAWDDSLS 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chicago
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                     us-09-315-574-60
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APPLICANT: Marks, James D.
APPLICANT: Schier, Robert
TITLE OF INVENTION: No. 6512097el High Affinity Human Antibodies to
TITLE OF INVENTION: Tumor Antigens
NUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESS:
ADDRESSEB: Majestic, Parsons, Siebert & Hsue P.C.
STRET: Four Embarcadero Center, Suite 1100
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                         ;
                                                                                                                                                                                                                                                                                                                                                                       Query Match 74.1%; Score 43; DB 2; Length 9; Best Local Similarity 100.0%; Pred. No. 4.1e+05; Matches 8; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/315,574
FILING DATE: 20-MAY-99
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
PRIOR APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
PRIOR APPLICATION NUMBER: US 60/000,250
FILING DATE: 13-JUN-1995
RICH APPLICATION NUMBER: US 08/665,202
APPLICATION NUMBER: US 08/665,202
RILING DATE: 13-JUN-1996
ATTONEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:

NAME: Hunter, Tom
REGISTRAINON NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061410
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Hunter, Tom
REGISTRATION NUMBER: 39,498
REFERENCE/DOCKET NUMBER: 02307E-061411
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JOHNAN TYPE: Floppy disk COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 60, Application US/09315574
Patent No. 6512097
                                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide US-08-665-202-60
                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 AAWDDSLS 8
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US-09-315-574-60
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Usery Marches Bit Conservative 10, Mismatches 0; Indels 0; Gaps 0; Matches Bit Conservative 0; Mismatches 0; Indels 0; Gaps 0; Matches Bit Conservative 0; Mismatches 0; Indels 0; Gaps 0; Matches Bit Conservative 0; Mismatches 0; Indels 0; Indels
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Gaps
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Nissim, Ahuva
Johnson, Kevin Stuart
Smith, Andrew John Hammond
TITLE OF INVENTION: Methods for producing members of specific
binding pairs
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/104,337A
FILING DATE: 25-Jun-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 600
CORRESPONDENCE ADDRESS:
ADDRESSEE: Audrey L. Bartnicki
STREET: Marchall, Gerstein & Borun
6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                    Length 10;
                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Bartnicki, Audrey L.
REGISTRATION NUMBER: 40,499
REFERENCE/DOCKET NUMBER: 28111/32372A
                                                                                                                                                                                                                                    Score 43; DB 2;
Pred. No. 0.15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 08/350,260
FILING DATE: 05-DEC-1994
APPLICATION NUMBER: GB 9110549.4
FILING DATE: 15-MAY-1991
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
APPLICATION NUMBER: PCT/GB92/00883
FILING DATE: 15-MAY-1992
APPLICATION NUMBER: PCT/GB93/00605
FILING DATE: 24-MAR-1993
APPLICATION NUMBER: US 08/150,002
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100.0%; Pred. No. v.-
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APPLICATION NUMBER: US 08/307,619
FILING DATE: 16-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 339, Application US/09104337A
Patent No. 6492160
GENERAL INFORMATION:
APPLICANT: Winter, Gregory Paul
Griffiths, Andrew David
Williams, Samuel Cameron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
INFORMATION FOR SEQ ID NO: 339:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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TELEPHONE: 312-474-6300
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                     single
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                                                                                                                                                                                                           Query Match
Best Local Similarity
Local 8; Conserve
                                                                                                    ; TYPE: amino acid
; STRANDEDNESS: Bir
; TOPOLOGY: linear
US-08-350-260A-497
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APPLICANT: Williams, Andrew David
APPLICANT: Williams, Samuel Cameron
APPLICANT: Williams, Samuel Cameron
APPLICANT: Wilsiam, Ahuva
APPLICANT: Johnson, Kevin Stuart
APPLICANT: Johnson, Kevin Stuart
APPLICANT: Smith, Andrew John Hammond
TITLE OF INVENTION: Methods for producing members of specific
TITLE OF INVENTION: binding pairs
NUMBER OF SEQUENCES: 602
CORRESPONDENCE ADDRESS:
ADDRESSEE: David W. Clough
STREET: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: Gloo Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
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MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Patchill Release #1.0, Version #1.25 (EPO)
SOFTWARE: Patchill Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/350,260A
FLING DATE: 0.5-DEC-1994
CLASSIFICATION DATA:
APPLICATION NUMBER: GB 9110549.4
FLING DATE: 15-MAY-1991
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
FILING DATE: 10-JUL-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB91/01134
FLING DATE: 10-JUL-1991
PRIOR APPLICATION DATA:
FILING DATE: 10-JUL-1991
PRIOR APPLICATION DATA:
FILING DATE: 15-MAY-1992
PRIOR APPLICATION DATA:
FILING DATE: 15-MAY-1992
PRIOR APPLICATION DATA:
FILING DATE: 24-MAR-1993
                                                                                                                                                          Length 10
                                                                                                                                                                                                              0; Indels
                                                                                                                                                          DB 2;
0.15;
                                                                                                                                                        74.1%; Score 43; DB 100.0%; Pred. No. 0.1; ive 0; Mismatches
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REGISTATION NUMBER: 36,107
REFERENCE,DOCKET NUMBER: 28111/32372
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 08/150,002
FILING DATE: 31-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/307,619
FILING DATE: 16-SEP-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-350-260A-497
; Sequence 497, Application US/08350260A
; Patent No. 5962255
  LENGTH: 10 amino acids
                                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 8; Conservative
                           TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                               1 AAWDDSLS 8
                                                                                                                                                                                                                                                                                                  1 AAWDDSLS 8
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US-08-350-260A-339
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; SEQUENCE DESCRIPTION: SEQ ID NO: 497:
US-09-104-337A-497
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER:
                                                                        Query Match
Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy o
                                                                                                                                                                  1 AAWDDSLS 8
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STATE: Illinois
COUNTRY: USA
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Smith, Andrew John Hammond
TITLE OF INVENTION: Methods for producing members of specific
binding pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUTER: FLOPEY GIRE
CONTUTER: FLOPEY GIRE
CONTUTER: FLOPEY GIRE
CONTUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/104,337A
FILING DATE: 05-DEC-1994
APPLICATION NUMBER: US 08/350,260
FILING DATE: 05-DEC-1994
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 15-MAX-1991
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAX-1992
APPLICATION NUMBER: PCT/GB92/00883
FILING DATE: 24-MAX-1992
APPLICATION NUMBER: PCT/GB92/00883
FILING DATE: 15-MAY-1993
APPLICATION NUMBER: US 08/150,002
FILING DATE: 15-MAX-1994
APPLICATION NUMBER: US 08/150,002
APPLICATION NUMBER: US 08/150,002
APPLICATION NUMBER: US 08/307,619
FILING DATE: 16-SEP-1994
ATTORNEY/AGENT INPORMATION: NUMBER: US 08/307,619
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ADDRESSEE: Audrey L. Bartnicki
STREET: Marshall, Gerstein & Borun
6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                        74.1%; Score 43; DB 4; Length 10; 100.0%; Pred. No. 0.15; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Bartnicki, Audrey L.
REGISTRATION NUMBER: 40,499
REFERENCE/DOCKET NUMBER: 28111/32372A
                                                                                                                                                                                                                                                                                                                                  RESULT 13
US-09-104-337A-497
; Sequence 497, Application US/09104337A
; Patent No. 6492160
; GENERAL INFORMATION:
; APPLICANT: Winter, Gregory Paul
Griffiths, Andrew David
; Williams, Samuel Cameron
; Waterhouse, Peter
; Waterhouse, Peter
; Nissim, Ahuva
    TYPE: amino acid
STRANDEDNESS: aingle
TOPOLGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 339:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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INFORMATION FOR SEQ ID NO: 497:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 anino acids
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Chicago
STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                         8; Conservative
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                                                                                                                                                                                                                                                                1 AAWDDSLS 8
                                                                                                                                                                Best Local Similarity
Matches 8; Conserv
                                                                                                US-09-104-337A-339
                                                                                                                                             Query Match
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Sequence 441, Application US/08350260A

Patent No. 5962255

GENERAL INFORMATION:
APPLICANT: Winter, Gregory Paul
APPLICANT: Williams, Samuel Cameron
APPLICANT: Williams, Peter
APPLICANT: Nissum, Ahuen
APPLICANT: Nissum, Ahuen
APPLICANT: Smith, Andrew John Hammond
TITLE OF INVENTION: Methods for producing members of specific
TITLE OF INVENTION: Methods for producing members of specific
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
SOFTWARE: PACHOLIN Release #1.0, Version #1.25 (EPO)
SOFTWARE: PACHOLIN NUMBER: US/08/350,260A
FILING DATE: 05-DEC-1994
CLASSIFICATION NUMBER: GB 9110549.4
FRIDR APPLICATION NUMBER: GB 9110549.4
FRIDR APPLICATION NUMBER: BCT/GB91/01134
APPLICATION NUMBER: PCT/GB91/01134
APPLICATION NUMBER: PCT/GB91/01134
APPLICATION NUMBER: PCT/GB92/00883
FILING DATE: 10-ULL-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB93/00605
FILING DATE: 10-ULL-1991
PRIOR APPLICATION NUMBER: DCT/GB93/00605
FILING DATE: 10-ULL-1991
PRIOR APPLICATION NUMBER: US 08/150,002
FILING DATE: 10-ULL-1994
APPLICATION NUMBER: US 08/307,619
FRIDR APPLICATION DATA:
APPLICATION NUMBER: US 08/307,619
FRIDR APPLICATION DATA:
APPLICATION NUMBER: US 08/307,619
FRIDR APPLICATION NUMBER: US 08/307,619
   Length 10;
                                                                      0; Indels
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STREET: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
   DB 4;
0.15;
74.1%; Score 43; DB 100.0%; Pred. No. 0.1 ative 0; Mismatches
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Job time : 21.6562 secs

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US-08-66-5-102-6
IS-08-66-5-102-6
IS-08-66-5-102-6
IS-08-66-5-102-6
IS-08-66-5-102-6
IS-08-66-5-102-6
IS-08-66-5-102-6
IS-08-68-102-6
INCOMMATION:
INTILE OF INVENTION:
INTELEPHONE:
INTILE OF INVENTION:
INTELEPHONE:
INTERPRETATION NUMBER:
INTILE OF INT
                                                                                                                                                                                                                                                                                            Gaps
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74.1%; Score 43; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 8; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                       Query Match 74.1%; Score 43; DB 2; Length 11; Best Local Similarity 100.0%; Pred. No. 0.17; Matches 8; Conservative 0; Mismatches 0; Indels
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-350-260A-441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 AAWDDSLS 8
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1 AAWDDSLS 8
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Search completed: October 14, 2005, 16:22:03

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Sequence 1927, Ap
Sequence 29, Appl
Sequence 33, Appl
Sequence 1926, Ap
Sequence 1926, Ap
Sequence 1926, Ap
Sequence 3241, Ap
Sequence 3241, Ap
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                                                                                                        October 14, 2005, 16:20:10 ; Search time 78.2031 Seconds (without alignments) 58.615 Million cell updates/sec
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Sequence 40,
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(ggn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
(ggn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-981-692-40
US-10-9880-748-1927
US-10-293-418-1927
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US-10-981-692-26
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        US-09-880-748-1917
        Sequence 1913, Ap Sequence 1917, Ap Sequence 1917, Ap 100.0
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        US-09-880-748-1917
        Sequence 1917, Ap Sequence 1917, Ap Sequence 1917, Ap 100.0
        246
        10
        US-09-880-748-1917
        Sequence 1917, Ap Sequence 1917, Ap Sequence 1917, Ap 100.0
        247
        10
        US-09-880-748-107
        Sequence 1917, Ap Sequence 1917, Ap Sequence 100.0
        247
        10
        US-09-880-748-107
        Sequence 1707, Ap Sequence 1928, Ap
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## ALIGNMENTS

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US-10-981-692-24

| Sequence 24, Application US/10981692 |
| Sequence 24, Application NS/10981692 |
| Sequence 24, Application NO. US20050163777A1 |
| GENERAL INFORMATION: Activition of the state of t
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Query Match
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US-10-981-692-29
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Sequence 40, Application US/10981692;
Publication No. US200S0163777A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION:
TITLE OF INVENTION: Antibodies that Specifically Bind to Neurokinin B
FILE REFERENCE: PF590P1
CURRENT APPLICATION NUMBER: 2004-11-05
PRIOR PILING DATE: 2003-05-29
PRIOR PILING DATE: 2003-05-29
PRIOR PILING DATE: 2003-05-30
PRIOR FILING DATE: 2002-05-30
NUMBER OF SEQ ID NOS: 76
SOFTWARE: PatentIn version 3.1
SEQ ID NO 40
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Publication No. US20030059937A1

GENERAL INFORMATION:

APPLICATY: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REFERENCE: PF523

CURRENT APPLICATION NUMBER: US/09/880,748

CURRENT APPLICATION NUMBER: 60/212,210

PRIOR APPLICATION NUMBER: 60/240,816

PRIOR PILING DATE: 2000-06-15

PRIOR PLING DATE: 2000-10-17

PRIOR PPLICATION NUMBER: 60/276,248

PRIOR PPLICATION NUMBER: 60/277,379

PRIOR PPLICATION NUMBER: 60/277,379

PRIOR PPLICATION NUMBER: 60/277,379

PRIOR PPLING DATE: 2001-03-16

PRIOR PLING DATE: 2001-03-16

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US-10-293-418-1927
US-quence 1927, Application US/10293418
; Publication No. US20030223996A1
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US-09-880-748-1927
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| Sequence 29, Application US/10981692
| Publication No. US2005016377A1
| GENERAL INFORMATION:
| APPLICANT: Rosen et al.
| TITLE OF INVENTION: Antibodies that Specifically Bind to Neurokinin B
| FILE REFERENCE: PF590P1
| CURRENT APPLICATION NUMBER: US/10/981,692
| FRIOR APPLICATION NUMBER: PCT/US03/16802
| PRIOR APPLICATION NUMBER: EC/383,802
| PRIOR APPLICATION NUMBER: 60/383,802
| PRIOR PILING DATE: 2002-05-30
| NUMBER OF SEQ ID NOS: 76
| SEQ ID NO 29
| LENGTH: 243
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100.0%; Score 58; DB 18; Length 243;
Best Local Similarity 100.0%; Pred. No. 0.048;
Matches 11; Conservative 0; Mismatches 0; Indels
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RESULT 6 US-10-981-692-33

2001-06-15

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CURRENT FILING DATE:
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LENGTH: 245
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; Sequence 33, Application US/10981692;
Publication No. US2005016377741;
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Antibodies that Specifically Bind to Neurokinin B FILE REFERENCE: PFS0P1
CURRENT FILING DATE: 2004-11-05;
PRIOR FILING DATE: 2004-11-05;
PRIOR FILING DATE: 2003-05-29;
PRIOR FILING DATE: 2002-05-30;
PRIOR FILING DATE: 2002-05-30;
NUMBER OF SEQ ID NOS: 76;
SEQ ID NO 33
LENGTH: 243
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| Sequence 26, Application US/10981692
| Sequence 26, Application US/10981692
| Publication US-0520050163777A1
| GENERAL INFORMATION:
| APPLICANT: Rosen et al. |
| TITLE OF INVENTION: Antibodies that Specifically Bind to Neurokinin B FILE REFERENCE: PFS90P1
| CURRENT APPLICATION NUMBER: US/10/981,692
| CURRENT APPLICATION NUMBER: US/10/981,692
| PRIOR PILING DATE: 2004-01-05, PRIOR PLICATION NUMBER: 60/383,802
| PRIOR FILING DATE: 2002-05-30
| NUMBER OF SEQ ID NOS: 76
| SEQ ID NO 26
| SEQ ID NO 26
| LENGTH: 244
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Publication No. US20030059937A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF523
CURRENT APPLICATION NUMBER: US/09/880,748
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Best Local Similarity 100.0%; Pred. No. 0.048;
Matches 11; Conservative 0; Mismatches 0; Indels
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; Pred. No. 0.048;
0; Mismatches 0; Indels
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US-10-981-692-26
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US-10-981-692-33
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Best Local Similarity 100.0%;
Matches 11; Conservative 0
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Sequence 1926, Application US/10293418

Publication No. US20030223996A1

GENERAL INFORMATION:

APPLICATY: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REFERENCE: PF523P2

CURRENT APPLICATION NUMBER: US/10/293,418

FILING DATE: 2001-11-27

PRIOR APPLICATION NUMBER: 60/331,469

PRIOR PILING DATE: 2001-11-16

PRIOR APPLICATION NUMBER: 60/340,817

PRIOR PILING DATE: 2001-01-6-15

PRIOR PILING DATE: 2001-06-15

PRIOR PILING DATE: 2001-06-15

PRIOR PILING DATE: 2001-06-15

PRIOR PILING DATE: 2001-03-16

PRIOR PILING DATE: 2001-03-16

PRIOR PILING DATE: 2001-01-7

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR PILING DATE: 2001-03-16

PRIOR PILING DATE: 2000-10-17

PRIOR PILING DATE: 2000-10-17

PRIOR PILING DATE: 2000-10-17

PRIOR PILING DATE: 2000-06-16

NUMBER OF SEQ ID NOS: 3247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 245;
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100.0%; Score 58; DB 10; Length 2
Best Local Similarity 100.0%; Pred. No. 0.048;
Matches 11; Conservative 0; Mismatches 0; Indels
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR PILING DATE: 2000-10-17
PRIOR PILING DATE: 2000-10-17
PRIOR PILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR PILING DATE: 2001-03-16
PRIOR PILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR PILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PATCHIN ON: 2.0
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Best Local Similarity 100.
Matches 11; Conservative
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US-10-293-418-1926
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US-09-880-748-1917
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                                                       GENERAL INVENTION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF523P2
CURRENT APPLICATION NUMBER: US/10/293,418
CURRENT APPLICATION NUMBER: 06/331,469
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/340,817
PRIOR APPLICATION NUMBER: 60/340,817
PRIOR PLILNG DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR PLILNG DATE: 2001-06-15
PRIOR PLILNG DATE: 2001-05-25
PRIOR PLILNG DATE: 2001-03-21
PRIOR PLILNG DATE: 2001-03-21
PRIOR PLING DATE: 2001-03-21
PRIOR PLING DATE: 2001-03-21
PRIOR PLING DATE: 2001-03-21
PRIOR PLING DATE: 2000-03-16
PRIOR PLILNG DATE: 2000-03-16
PRIOR PLILNG DATE: 2000-01-17
PRIOR PLILNG DATE: 2000-10-17
PRIOR PLILNG DATE: 2000-10-17
PRIOR PLILNG DATE: 2000-11-17
PRIOR PLING DATE: 2000-11-17
PRIOR PLILNG DATE: 2000-11-17
PRIOR PLING DATE: 2000
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TITLE OF INVENTION: Attibodies that Specifically Bind to Neurokinin E TITLE OF INVENTION: Attibodies that Specifically Bind to Neurokinin E CURRENT APPLICATION NUMBER: US/10/981,692
CURRENT FILING DATE: 2004-11-05
PRIOR APPLICATION NUMBER: PCT/US03/16802
PRIOR PILING DATE: 2003-05-29
PRIOR PILING DATE: 2002-05-30
PRIOR FILING DATE: 2002-05-30
SUMBER OF SEC ID NOS: 76
SOFTWARE: Patentin version 3.1
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; Sequence 31, Application US/10981692
; Publication No. US20050163777A1
; GENERAL INFORMATION:
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ORGANISM: Artificial sequence
Publication No. US20030223996A1
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US-10-293-418-3241
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LENGTH: 245
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; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVERFICE PF53
; TIER REPERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT PILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR FILING DATE: 2000-06-15
; PRIOR FILING DATE: 2000-10-17
; PRIOR PELICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2001-03-16
; PRIOR FILING DATE: 2001-03-16
; PRIOR FILING DATE: 2001-03-16
; PRIOR PILING DATE: 2001-03-21
; PRIOR PILING DATE: 2001-03-21
; PRIOR PILING DATE: 2001-03-21
; PRIOR PILING DATE: 2001-03-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PRECEITING VET. 2.0
; SEQ ID NO 1913
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100.0%; Score 58; DB 10; Length 246;
Best Local Similarity 100.0%; Pred. No. 0.049;
Matches 11; Conservative 0; Mismatches 0; Indels (
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Best Local Similarity luv.
Best Local 11, Conservative
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CORGANISM: Homo sapiens
US-09-880-748-1917
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CORGANISM: Homo sapiens
US-09-880-748-1913
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RESULT 12

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Length 246; 0; Indels

100.0%; Score 58; DB 15; 100.0%; Pred. No. 0.049; 0; Mismatches

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WESULT 1933, 418-1913

Sequence 1913, Application US/10293418

POLICARIA NO. USZO00223996A1

GENERAL INFORMATION:

TITLE OF INFORMATION: Antibodies that Immunospecifically Bind BLyS

TITLE OF INFORMATION: Antibodies that Immunospecifically Bind BLyS

CURRENT PILING DATE: 2002-11-27

PRIOR APPLICATION NUMBER: 06/340,817

PRIOR APPLICATION NUMBER: 60/340,817

PRIOR PILING DATE: 2001-11-16

PRIOR PILING DATE: 2001-06-15

PRIOR PILING DATE: 2001-06-15

PRIOR PILING DATE: 2001-06-25

PRIOR PILING DATE: 2001-05-25

PRIOR PILING DATE: 2001-05-26

PRIOR PILING DATE: 2001-03-21

PRIOR PILING DATE: 2001-03-21

PRIOR PILING DATE: 2001-03-21

PRIOR PILING DATE: 2001-03-16

PRIOR PILING DATE: 2001-03-16

PRIOR PILING DATE: 2001-03-16

PRIOR PILING DATE: 2001-01-17

PRIOR PILING DATE: 2001-03-16

PRIOR PILING DATE: 2001-01-17

PRIOR PILING DATE: 2001-01-17

PRIOR PILING DATE: 2000-10-17

PRIOR PILING DATE: 2000-10-17

PRIOR PILING DATE: 2000-6-16

NUMBER OF SEQ ID NOS: 3247
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Sequence 1917, Application US/10293418

Publication No. US2003022996A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

CURRENT FILING DATE: 2002-11-27

PRIOR APPLICATION NUMBER: 06/331,469

PRIOR PILING DATE: 2001-12-19

PRIOR APPLICATION NUMBER: 06/340,817

PRIOR APPLICATION NUMBER: 06/293,499

PRIOR PILING DATE: 2001-06-15

PRIOR FILING DATE: 2001-06-15

PRIOR FILING DATE: 2001-06-15

PRIOR FILING DATE: 2001-03-16

PRIOR PILING DATE: 2000-06-16

PRIOR PILING DATE: 2000-06-16
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Best Local Similarity 100.
Matches 11; Conservative
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; ORGANISM: Homo sapiens
US-10-293-418-1913
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ORGANISM: Homo sapiens
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Search completed: October 14, 2005, 17:00:44 Job time : 78.2031 secs
                       Query Match
Best Local Similarity 100.
Matches 11, Conservative
                                                                                                                225 AAWDDSLSEFL 235
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US-10-293-418-1917
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